

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:03:24 ; Search time 166 Seconds
(without alignments)
766.531 Million cell updates/sec

Title: us-10-687-268-35

Perfect score: 1756

Sequence: 1 MVTKAFVLLAFAEASAKSC.....YFSDVLHLLIMLIGICAVL 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1756	100.0	329	5	Aae17314 Human tec
2	1756	100.0	329	5	Adh48858 NOV60C pr
3	1756	100.0	329	8	Adh72158 Human pro
4	1751	99.7	329	5	Adh48856 NOV60B pr
5	1751	99.7	329	8	Adh72162 Human pro
6	1539.5	87.7	300	5	Adh48854 NOV60A pr
7	1539.5	87.7	300	8	Adh72160 Human pro
8	1505	85.7	276	8	Adh72164 Human pro
9	1478	84.2	273	8	Adh72166 Human pro
10	248	14.1	415	5	Abg72418 Cytochrom
11	228.5	13.0	644	8	Ado59937 Rat UMOD
12	223.5	12.7	642	8	Ado59936 Murine UM
13	222	12.6	621	8	Abm82705 Human dia
14	221	12.6	640	8	Abm82704 Human dia
15	220	12.5	643	8	Ado59935 Bovine UM
16	219	12.5	507	8	Adr09416 Human pro
17	219	12.5	577	7	Adm04800 Human pro
18	219	12.5	673	7	Adb64620 Human pro
19	213	12.1	406	3	Aab54274 Human pan
20	210	12.0	527	8	Adi02916 Human pan
21	210	12.0	530	5	Aae17559 Human pan
22	210	12.0	534	6	AbR39945 Human pro
23	210	12.0	640	8	Ado59934 Human UMO
24	210	12.0	640	8	Adt49902 Human UMO
25	209	11.9	384	2	Aar98963 Human GP2

ALIGNMENTS

RESULT 1

AAE17314

ID AAE17314 standard; protein; 329 AA.

XX AC AAE17314;

XX AC AAE17314;

DT 18-APR-2002 (first entry)

DE Human tectorin beta protein, sbg453915TECTORINA.

XX Human; therapy; wound healing disorder; vaccine; cancer; infection;

KW autoimmunity disorder; haematopoietic disorder; inflammation; arthritis;

KW Parkinson's disease; Huntington's chorea; schizophrania; antiarrhythmic;

KW multiple sclerosis; Alzheimer's disease; analgesic; cardiac; asthma;

KW ischaemia; stroke; AIDS; bone disease; atherosclerosis; brain disorder;

KW depression; cardiovascular disease; myocardial infarction; renal failure;

KW respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder;

KW type II diabetes mellitus; skeletal muscle disorder; immunosuppressive;

KW hyperplasia; renal disease; hypoglycaemia; gastrointestinal disease;

KW neotrophic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;

KW haemostatic; vulnery; anticonvulsant; antirheumatic; neuroprotective;

KW nephrotropic; hypotensive; vasotrophic; cytostatic; cerebroprotective;

KW allergy; tectorin beta.

XX Homo sapiens.

XX WO200198342-A1.

XX 27-DEC-2001.

XX 22-JUN-2001; 2001WO-US019929.

XX 22-JUN-2000; 2000US-0213156P.

XX 22-JUN-2000; 2000US-0213161P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX (GLAX) GLAXO GROUP LTD.

XX Agarwal P, Cogswell JP, Kabnic KS, Lai Y, Martensen SA;

XX Murdock PR, Smith RF, Strum JC, Xiang Z, Xie Q, Rizni SK;

XX WPI; 2002-139783/18.

XX N-FSDB; AAD27809.

XX Novel secreted and membrane-associated polypeptides and polynucleotides

XX useful for preventing, ameliorating or correcting dysfunction or disease

XX including diabetes, cancer, hypertension and growth abnormalities.

26	198.5	11.3	499	8	ABM84563	Human dia
27	198.5	11.3	499	8	ABM84554	Human dia
28	198.5	11.3	499	8	ABM84557	Human dia
29	198.5	11.3	499	8	ABM84562	Human dia
30	188.5	10.7	668	8	ABM82703	Human dia
31	182	10.4	413	7	ADF17467	Mouse li-
32	181.5	10.3	607	5	AAG77919	Rat oestr
33	181.5	10.3	607	5	AAAM49027	Human uro
34	178.5	10.2	1246	6	ABB98302	Human uro
35	174	9.9	620	7	ADM47277	Protocadh
36	173.5	9.9	1011	6	ABJ19385	NOVX rela
37	173.5	9.9	1011	6	ADO41770	Novel hum
38	172	9.8	248	8	ADO41778	Novel hum
39	172	9.8	585	3	AAAB07456	Protein e
40	172	9.8	585	5	AAE25856	Human pro
41	172	9.8	600	6	ADA57143	Human sec
42	172	9.8	600	6	ADA41006	Human sec
43	172	9.8	607	2	AAAY13377	Amino aci
44	172	9.8	607	2	AAAY25323	Human pan
45	172	9.8	607	3	ADC78510	Human PRO

Brannock, M,
101687268
Seq. ID 35

XX PS Claim 1; Page 127-128; 138pp; English.

XX CC The invention relates to secreted and membrane-associated polypeptides and polynucleotides. The sequences of the invention are useful in

XX CC diagnostic assays for detecting diseases associated with inappropriate

XX CC activity or levels of these polynucleotides, and in identifying their

XX CC agonists and antagonists that are potentially useful in inducing

XX CC sequences of the invention are useful as vaccines for

XX CC immunological response. The sequences of the invention are useful for

XX CC treating cancers, infections, autoimmune disorders, haematopoietic

XX CC disorders, wound healing disorders, cholesterol ester storage disease,

XX CC inflammation, congenital muscular dystrophy, junctional epidermolysis

XX CC bullosa, Parkinson's disease, Huntington's chorea, multiple sclerosis,

XX CC viral and bacterial infections, Alzheimer's disease, asthma, arthritis,

XX CC allergies, schizophrenia, sbg4445PROA-associated disorders,

XX CC septicemia, psoriasis, inflammatory bowel disease, transplant rejection,

XX CC graft versus host disease, ischaemia, stroke, acute respiratory disease

XX CC syndrome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis,

XX CC brain disorders including paraneoplastic palsy, myotonic dystrophy,

XX CC depression, anxiety disorders and sleep disorders, cardiovascular

XX CC diseases including congestive heart failure and myocardial infarction,

XX CC respiratory diseases including chronic obstructive pulmonary disease,

XX CC acute bronchitis and adult respiratory distress syndrome, liver disorders

XX CC including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral

XX CC and non-viral hepatitis, type II diabetes mellitus, renal disease

XX CC including acute and chronic renal failure, glomerulonephritis, Fanconi's

XX CC syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia

XX CC and tendinitis, gastrointestinal diseases including intestinal

XX CC obstruction and tropical sprue, spleen disorders including hypersplenism,

XX CC Hodgkin's disease and malignant lymphoma, testicular cancer, male

XX CC reproductive diseases including low testosterone and male infertility.

XX CC The present sequence is human tectorin beta protein

XX CC Sequence 329 AA;

XX CC Query Match 100.0%; Score 1756; DB 5; Length 329;

XX CC Best Local Similarity 100.0%; Pred. No. 1.8e-180; Indels 0; Gaps 0;

XX CC Matches 329; Conservative 0; Mismatches 0;

QY 1 MYTKAFVLLAIFAEASAKSCAPNKADVLVFCYPKTITIKIPECPYGVHQLAGGLCY 60

DB 1 MYTKAFVLLAIFAEASAKSCAPNKADVLVFCYPKTITIKIPECPYGVHQLAGGLCY 60

QY 61 NGVHEGGYQFVLPDLPKNSYCGTQSEYKPPYHVFYSHIVSNDTIVIKNQPVNYSFS 120

DB 61 NGVHEGGYQFVLPDLPKNSYCGTQSEYKPPYHVFYSHIVSNDTIVIKNQPVNYSFS 120

QY 121 CTVHSTYLVNQAFDQVATVHVKNMGSTFESQSLNFTYTNKFSIKKEAPFVLEAEI 180

DB 121 CTVHSTYLVNQAFDQVATVHVKNMGSTFESQSLNFTYTNKFSIKKEAPFVLEAEI 180

QY 181 GSDLFAGVEAKGLSIRFKVVLNSCWATPSADFWYPLQWLKNGCPTDTVLVHNGRDH 240

DB 181 GSDLFAGVEAKGLSIRFKVVLNSCWATPSADFWYPLQWLKNGCPTDTVLVHNGRDH 240

QY 241 RATPFQNAFPQNPVKLSKVLHCEFTFICDSEKLSCPVTCDDRKLRLDQTGGVLVWELS 300

DB 241 RATPFQNAFPQNPVKLSKVLHCEFTFICDSEKLSCPVTCDDRKLRLDQTGGVLVWELS 300

QY 301 LRSRGFSSLYSFSQVLLHLMGLICAVL 329

DB 301 LRSRGFSSLYSFSQVLLHLMGLICAVL 329

RESULT 2

ADH48858

ID ADH48858 standard; protein; 329 AA.

XX ADH48858;

XX ADH48858;

DT 25-MAR-2004 (first entry)

XX

DE NOV60C protein sequence, SEQ ID 142.

XX Human; NOVX; atherosclerosis; hypertension; obesity; cancer; cytostatic;

XX KW hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV60C;

XX KW beta tectorin-like protein; chromosome 10.

OS Homo sapiens.

OS WO200268652-A2.

XX 06-SEP-2002.

XX 26-FEB-2002; 2002WO-US005910.

XX 26-FEB-2001; 2001US-0271646P.

XX 27-FEB-2001; 2001US-0271840P.

XX 28-FEB-2001; 2001US-0272404P.

XX 28-FEB-2001; 2001US-0272405P.

XX 28-FEB-2001; 2001US-0272410P.

XX 28-FEB-2001; 2001US-0272414P.

XX 02-MAR-2001; 2001US-0272787P.

XX 02-MAR-2001; 2001US-0272922P.

XX 02-MAR-2001; 2001US-0273048P.

XX 02-MAR-2001; 2001US-0273300P.

XX 16-MAR-2001; 2001US-0276401P.

XX 20-MAR-2001; 2001US-0277324P.

XX 20-MAR-2001; 2001US-0278660P.

XX 30-MAR-2001; 2001US-0280039P.

XX 30-MAR-2001; 2001US-0280234P.

XX 02-APR-2001; 2001US-0280818P.

XX 12-APR-2001; 2001US-0283443P.

XX 23-APR-2001; 2001US-0285754P.

XX 24-APR-2001; 2001US-0286096P.

XX 03-MAY-2001; 2001US-0288353P.

XX 17-MAY-2001; 2001US-0291703P.

XX 31-MAY-2001; 2001US-0294834P.

XX 20-JUN-2001; 2001US-0296959P.

XX 21-JUN-2001; 2001US-0298454P.

XX 05-JUL-2001; 2001US-0303242P.

XX 13-AUG-2001; 2001US-0311981P.

XX 16-AUG-2001; 2001US-0312858P.

XX 17-AUG-2001; 2001US-0313280P.

XX 29-AUG-2001; 2001US-0315614P.

XX 17-SEP-2001; 2001US-0322818P.

XX 25-FEB-2002; 2002US-00322818.

XX (CURA-) CURAGEN CORP.

XX Alsobrook JP, Anderson DW, Ballinger RA, Boldog FL, Burgess CE;

XX Caeman SJ, Ellerman KB, Gangolli EA, Gerlach VL, Gilbert JA;

XX Gorman L, Guo X, Gusev YV, Kekuda R, Li L, Liu X, Malyankar UM;

XX Miller CE, Millet I, Padigaru M, Patcurajan M, Pena CEA, Feyman JA;

XX Rastelli L, Shenoy SG, Shimkets RA, Smithson G, Spytek KA, Stone DJ;

XX Taupier RJ, Tchernov VT, Vernet CAM, Zethusen BD;

XX WPI; 2002-698672/75.

XX N-PSDB; ADH48857.

XX New NOVX polypeptides or polynucleotides, useful for preventing or

XX treating disorders or syndromes e.g., atherosclerosis, hypertension,

XX obesity or cancer.

XX Claim 1; Page 338; 923pp; English.

XX The present invention relates to novel human NOVX proteins, where X is

XX any number from 1 to 91 and their coding sequences. The proteins and

XX coding sequences are useful for preventing or treating disorders or

XX syndromes e.g. atherosclerosis, hypertension, obesity or cancer. NOV60 is

XX a beta tectorin-like protein and its coding sequence maps to chromosome

XX 10.

XX Sequence 329 AA;

Query Match		100.0%; Score 1756; DB 5; Length 329;
-Best Local Similarity		100.0%; Pred. No. 1.8e-180;
Matches 329; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MTKAPVLLAI PAEASAKSCAPNKADVILVFCYPKTIIKIPECYPGWVHQLALGGLCY 60
DB	1	MTKAPVLLAI PAEASAKSCAPNKADVILVFCYPKTIIKIPECYPGWVHQLALGGLCY 60
QY	61	NGVHEGGYQFVLPDLSPPNKSYCGTQSYKPKPIYHFYSHIVSNDTIVVKQPNVNSFS 120
DB	61	NGVHEGGYQFVLPDLSPPNKSYCGTQSYKPKPIYHFYSHIVSNDTIVVKQPNVNSFS 120
QY	121	CTYHSTYLVNQAFDORVATVHVKGSMGTFFSQSLNFTYTNAKFSIKKEAPFVLEASI 180
DB	121	CTYHSTYLVNQAFDORVATVHVKGSMGTFFSQSLNFTYTNAKFSIKKEAPFVLEASI 180
QY	181	GSDLFAGVEAKGLSTRFKVILNSCWATPSADFMYPLOWQILNKGCPTDTEVLVHNGRDH 240
DB	181	GSDLFAGVEAKGLSTRFKVILNSCWATPSADFMYPLOWQILNKGCPTDTEVLVHNGRDH 240
QY	241	RATFQNAFRFQNI PKLSKVWLHCETFCIDSEKLSCPVTCDKRKRLLRDQDTGGVLVVELS 300
DB	241	RATFQNAFRFQNI PKLSKVWLHCETFCIDSEKLSCPVTCDKRKRLLRDQDTGGVLVVELS 300
QY	301	LRSRGFSLSYFSDVHLHLMGLICAVL 329
DB	301	LRSRGFSLSYFSDVHLHLMGLICAVL 329
RESULT 3		
ID	ADH72158	standard; protein; 329 AA.
XX	ADH72158;	
XX	25-MAR-2004	(first entry)
DE	Human protein of the invention NOV48a SEQ ID NO:1054.	
KW	human; cytostatic; immunomodulator; neuroprotective; nootropic;	
KW	anorectic; antididiabetic; antimicrobial; antilipemic; gene therapy;	
KW	vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;	
KW	obesity; diabetes; infectious disease; metabolic syndrome X;	
KW	dyslipidaemia.	
OS	Homo sapiens.	
XX	WO2003102155-A2.	
XX	11-DEC-2003.	
XX	03-JUN-2003; 2003WO-05017430.	
XX	03-JUN-2002; 2002US-03851208.	
XX	04-JUN-2002; 2002US-0385784P.	
XX	05-JUN-2002; 2002US-0386041P.	
XX	05-JUN-2002; 2002US-0386047P.	
XX	06-JUN-2002; 2002US-0386376P.	
XX	06-JUN-2002; 2002US-0386453P.	
XX	06-JUN-2002; 2002US-0386864P.	
XX	06-JUN-2002; 2002US-0387016P.	
XX	07-JUN-2002; 2002US-0386796P.	
XX	07-JUN-2002; 2002US-0386816P.	
XX	07-JUN-2002; 2002US-0386931P.	
XX	07-JUN-2002; 2002US-0386942P.	
XX	07-JUN-2002; 2002US-0386971P.	
XX	07-JUN-2002; 2002US-0387262P.	
XX	08-JUN-2002; 2002US-0296960P.	
XX	10-JUN-2002; 2002US-0387400P.	
XX	10-JUN-2002; 2002US-0387535P.	
XX	11-JUN-2002; 2002US-0387610P.	
XX	11-JUN-2002; 2002US-0387625P.	
XX	11-JUN-2002; 2002US-0387634P.	

PR	11-JUN-2002; 2002US-0387668P.	
PR	11-JUN-2002; 2002US-0387696P.	
PR	11-JUN-2002; 2002US-0387702P.	
PR	11-JUN-2002; 2002US-0387836P.	
PR	11-JUN-2002; 2002US-0387859P.	
PR	12-JUN-2002; 2002US-0387933P.	
PR	12-JUN-2002; 2002US-0387934P.	
PR	12-JUN-2002; 2002US-0387960P.	
PR	12-JUN-2002; 2002US-0388022P.	
PR	12-JUN-2002; 2002US-0388096P.	
PR	13-JUN-2002; 2002US-0389123P.	
PR	14-JUN-2002; 2002US-0389118P.	
PR	14-JUN-2002; 2002US-0389120P.	
PR	14-JUN-2002; 2002US-0389144P.	
PR	14-JUN-2002; 2002US-0389146P.	
PR	17-JUN-2002; 2002US-0389729P.	
PR	17-JUN-2002; 2002US-0389742P.	
PR	18-JUN-2002; 2002US-0389884P.	
PR	19-JUN-2002; 2002US-0390066P.	
PR	19-JUN-2002; 2002US-0390209P.	
PR	21-JUN-2002; 2002US-0390763P.	
PR	17-JUL-2002; 2002US-0396706P.	
PR	06-AUG-2002; 2002US-0401628P.	
PR	09-AUG-2002; 2002US-0402156P.	
PR	09-AUG-2002; 2002US-0402256P.	
PR	09-AUG-2002; 2002US-0402389P.	
PR	12-AUG-2002; 2002US-0402786P.	
PR	12-AUG-2002; 2002US-0402816P.	
PR	12-AUG-2002; 2002US-0402821P.	
PR	12-AUG-2002; 2002US-0402832P.	
PR	13-AUG-2002; 2002US-0403448P.	
PR	13-AUG-2002; 2002US-0403459P.	
PR	13-AUG-2002; 2002US-0403531P.	
PR	13-AUG-2002; 2002US-0403532P.	
PR	13-AUG-2002; 2002US-0403563P.	
PR	15-AUG-2002; 2002US-0403617P.	
PR	26-AUG-2002; 2002US-0406182P.	
PR	26-AUG-2002; 2002US-0406355P.	
PR	27-AUG-2002; 2002US-0406240P.	
PR	12-SEP-2002; 2002US-0410084P.	
PR	20-SEP-2002; 2002US-0412528P.	
PR	23-SEP-2002; 2002US-0412731P.	
PR	30-SEP-2002; 2002US-0414801P.	
PR	30-SEP-2002; 2002US-0414839P.	
PR	30-SEP-2002; 2002US-0414840P.	
PR	30-SEP-2002; 2002US-0414954P.	
PR	09-OCT-2002; 2002US-0417186P.	
PR	09-OCT-2002; 2002US-0417406P.	
PR	23-OCT-2002; 2002US-0420639P.	
PR	28-OCT-2002; 2002US-0421156P.	
PR	31-OCT-2002; 2002US-0422690P.	
PR	01-NOV-2002; 2002US-0423130P.	
PR	05-NOV-2002; 2002US-00423798.	
PR	05-NOV-2002; 2002US-0423798P.	
XX	12-NOV-2002; 2002US-0425453P.	
PA	(CURA-) CURAGEN CORP.	
XX	Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;	
PI	Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;	
PI	Eitenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;	
PI	Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;	
PI	MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;	
PI	Padigara M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;	
PI	Riesger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;	
PI	Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;	
XX	Zhong H;	
DR	WPI; 2004-081935/08.	
DR	N-PSDB; ADH72157.	
XX		
PT	New NOVX polypeptides and nucleic acid molecules useful for preventing or	

PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
 PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Example 48; SEQ ID NO 1054; 1880pp; English.
 XX
 CC The invention relates to a novel isolated polypeptide (NOVX). A
 CC polypeptide of the invention has cytostatic, immunomodulator,
 CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
 CC antilipemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC represents a NOVX polypeptide of the invention.
 XX
 SQ Sequence 329 AA;

Query Match 100.0%; Score 1756; DB 8; Length 329;
 Best Local Similarity 100.0%; Pred. No. 1.8e-180;
 Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGVHQLALGGLCY 60
 DB 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGVHQLALGGLCY 60

. QY 61 NGVHEGGYQFVLPDLSFNKSYCGTQSEYKPPYHFSYHVSNDTIVVKNQPNYSFS 120
 DB 61 NGVHEGGYQFVLPDLSFNKSYCGTQSEYKPPYHFSYHVSNDTIVVKNQPNYSFS 120

QY 121 CTHYSTYLVNQAAFDQVATVHVKNKSGMTFESQLSLNFYTNKTSIKKEAPFVLEASEI 180
 DB 121 CTHYSTYLVNQAAFDQVATVHVKNKSGMTFESQLSLNFYTNKTSIKKEAPFVLEASEI 180

QY 181 GSDLPAGVEAKGLSIRFKVNLNSCWATPSADFMYPLOQLINKGCPDTETVLVHNGRDH 240
 DB 181 GSDLPAGVEAKGLSIRFKVNLNSCWATPSADFMYPLOQLINKGCPDTETVLVHNGRDH 240

QY 241 RATFQNAFRFQNIPLSKVNLHCETFFICDSKLSCPVTCDFKRLRDQTGGVLVLELS 300
 DB 241 RATFQNAFRFQNIPLSKVNLHCETFFICDSKLSCPVTCDFKRLRDQTGGVLVLELS 300

QY 301 LRSRGFSSLYSFDVLHLLIMLIGICAVL 329
 DB 301 LRSRGFSSLYSFDVLHLLIMLIGICAVL 329

RESULT 4
 ADH48856
 ID ADH48856 standard; protein; 329 AA.
 XX
 AC ADH48856;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE NOV60B protein sequence, SEQ ID 140.
 XX
 KW Human; NOVX; atherosclerosis; hypertension; obesity; cancer; cytostatic;
 KW hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV60B;
 KW beta tectorin-like protein; chromosome 10.
 XX
 OS Homo sapiens.
 XX
 FN WO200268652-A2.
 XX
 PD 06-SEP-2002.
 XX
 PP 26-FEB-2002; 2002WO-US0005910.

XX 26-FEB-2001; 2001US-0271646P.
 PR 27-FEB-2001; 2001US-0271840P.
 PR 28-FEB-2001; 2001US-0272404P.
 PR 28-FEB-2001; 2001US-0272405P.
 PR 28-FEB-2001; 2001US-0272410P.
 PR 28-FEB-2001; 2001US-0272414P.
 PR 02-MAR-2001; 2001US-0272787P.
 PR 02-MAR-2001; 2001US-0272922P.
 PR 02-MAR-2001; 2001US-0273048P.
 PR 02-MAR-2001; 2001US-0273300P.
 PR 16-MAR-2001; 2001US-0276401P.
 PR 20-MAR-2001; 2001US-0277324P.
 PR 20-MAR-2001; 2001US-0278650P.
 PR 30-MAR-2001; 2001US-0280039P.
 PR 30-MAR-2001; 2001US-0280234P.
 PR 02-APR-2001; 2001US-0280818P.
 PR 12-APR-2001; 2001US-0283443P.
 PR 23-APR-2001; 2001US-0285754P.
 PR 24-APR-2001; 2001US-0286096P.
 PR 03-MAY-2001; 2001US-0288353P.
 PR 17-MAY-2001; 2001US-0291703P.
 PR 31-MAY-2001; 2001US-0294834P.
 PR 20-JUN-2001; 2001US-0299695P.
 PR 21-JUN-2001; 2001US-0299845P.
 PR 05-JUL-2001; 2001US-0303242P.
 PR 13-AUG-2001; 2001US-0311981P.
 PR 16-AUG-2001; 2001US-0312858P.
 PR 17-AUG-2001; 2001US-0313280P.
 PR 29-AUG-2001; 2001US-0315614P.
 PR 17-SEP-2001; 2001US-0322818P.
 PR 25-FEB-2002; 2002US-00322818.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Alsbrook JP, Anderson DW, Ballinger RA, Boldog FL, Burgess CE;
 PI Casman SJ, Ellerman KE, Gangolli EA, Gerlach VL, Gilbert JA;
 PI Gorman L, Guo X, Gusev VY, Kekuda R, Li L, Liu X, Malyankar UM;
 PI Miller CE, Millet I, Padigaru M, Patturajan M, Pena CEA, Peyman JA;
 PI Rastelli L, Shenoy SG, Shimkets RA, Smithson G, Spytek KA, Stone DJ;
 PI Taupier RJ, Tchernev VT, Vernet CAM, Zethusen BD;
 XX
 DR WPI; 2002-698672/75.
 DR N-PSDB; ADH48855.
 XX
 PT New NOVX polypeptides or polynucleotides, useful for preventing or
 PT treating disorders or syndromes e.g., atherosclerosis, hypertension,
 PT obesity or cancer.
 XX
 PS Claim 1; Page 336; 923pp; English.
 XX
 CC The present invention relates to novel human NOVX proteins, where X is
 CC any number from 1 to 91 and their coding sequences. The proteins and
 CC coding sequences are useful for preventing or treating disorders or
 CC syndromes e.g. atherosclerosis, hypertension, obesity or cancer. NOV60 is
 CC a beta tectorin-like protein and its coding sequence maps to chromosome
 CC 10.
 XX
 SQ Sequence 329 AA;

Query Match 99.7%; Score 1751; DB 5; Length 329;
 Best Local Similarity 99.7%; Pred. No. 6.4e-180;
 Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGVHQLALGGLCY 60
 DB 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGVHQLALGGLCY 60

QY 61 NGVHEGGYQFVLPDLSFNKSYCGTQSEYKPPYHFSYHVSNDTIVVKNQPNYSFS 120
 DB 61 NGVHEGGYQFVLPDLSFNKSYCGTQSEYKPPYHFSYHVSNDTIVVKNQPNYSFS 120

QY 121 CTHYSTYLVNQAAFDQVATVHVKNKSGMTFESQLSLNFYTNKTSIKKEAPFVLEASEI 180

Db 121 CTHSTYLVNQAFDQVATVHVYKNGSMGTFESQLSINFTYNAKFSIKKEAPFVLEASFI 180
QY 181 GSDLFAGVAKGLSIRFKVVLNSCWATPSADFMYPLOWOLINKGCPDTETVLVHENGDRH 240
Db 181 GSDLFAGVAKGLSIRFKVVLNSCWATPSADFMYPLOWOLINKGCPDTETVLVHENGDRH 240
QY 241 RATFQFNAPFRFQNIPLKSKVWLHCETFCIDSEKLSCPVTCDKRKLRLRDTQGGVLVVELS 300
Db 241 RATFQFNAPFRFQNIPLKSKVWLHCETFCIDSEKLSCPVTCDKRKLRLRDTQGGVLVVELS 300
QY 301 LRSRGFSSLYSPSDVLHLLHMLGICAVL 329
Db 301 LRSRGFSSLYSPSDVLHLLHMLGICAVL 329
RESULT 5
ADH72162
ID ADH72162 standard; protein; 329 AA.
AC ADH72162;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human protein of the invention NOV48c SEQ ID NO:1058.
XX human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
OS Homo sapiens.
XX
PN WO2003102155-A2.
PD
PP 11-DEC-2003.
PP
PP 03-JUN-2003; 2003WO-US017430.
PP
PP 03-JUN-2002; 2002US-0385120P.
PP 04-JUN-2002; 2002US-0385784P.
PP 05-JUN-2002; 2002US-0386041P.
PP 05-JUN-2002; 2002US-0386047P.
PP 06-JUN-2002; 2002US-0386376P.
PP 06-JUN-2002; 2002US-0386453P.
PP 06-JUN-2002; 2002US-0386864P.
PP 06-JUN-2002; 2002US-0387016P.
PP 07-JUN-2002; 2002US-0386796P.
PP 07-JUN-2002; 2002US-0386816P.
PP 07-JUN-2002; 2002US-0386931P.
PP 07-JUN-2002; 2002US-0386942P.
PP 07-JUN-2002; 2002US-0386971P.
PP 07-JUN-2002; 2002US-0387262P.
PP 08-JUN-2002; 2002US-0296960P.
PP 10-JUN-2002; 2002US-0387400P.
PP 10-JUN-2002; 2002US-0387535P.
PP 11-JUN-2002; 2002US-0387610P.
PP 11-JUN-2002; 2002US-0387625P.
PP 11-JUN-2002; 2002US-0387634P.
PP 11-JUN-2002; 2002US-0387668P.
PP 11-JUN-2002; 2002US-0387696P.
PP 11-JUN-2002; 2002US-0387702P.
PP 11-JUN-2002; 2002US-0387836P.
PP 11-JUN-2002; 2002US-0387859P.
PP 12-JUN-2002; 2002US-0387933P.
PP 12-JUN-2002; 2002US-0387934P.
PP 12-JUN-2002; 2002US-0387960P.
PP 12-JUN-2002; 2002US-0388022P.
PP 12-JUN-2002; 2002US-0388096P.
PP 13-JUN-2002; 2002US-0389123P.
PP 14-JUN-2002; 2002US-0389118P.
PP 14-JUN-2002; 2002US-0389120P.

PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402158P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 12-SEP-2002; 2002US-0406240P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
MacLachlan T, Malyankar UM, Merick AJ, Millet I, Mishra VS;
Padigaru M, Patturajan M, Pena CE, Feyman JA, Raha D, Rastelli L;
Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
Zhong H;
WPI: 2004-081935/08.
DR N-PSDB; ADH72161.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
PT
XX Example 48; SEQ ID NO 1058; 1880pp; English.
PS
XX The invention relates to a novel isolated polypeptide (NOVX). A
polypeptide of the invention has cytostatic, immunomodulator,
neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
antilipemic activity, and may have a use in gene therapy, and as a
vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
any of the 303 fully defined nucleotide sequences given in the
specification. The polypeptide is useful in the manufacture of a
medicament for treating a syndrome associated with a human disease. The

CC polypeptide, polynucleotide and antibody are useful in diagnosing.
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC represents a NOVX polypeptide of the invention.
 XX
 - SQ Sequence 329 AA;
 Query Match 99.7%; Score 1751; DB 8; Length 329;
 Best Local Similarity 99.7%; Pred. No. 6.4e-180;
 Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGVHQLALGGLCY 60
 Db 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGVHQLALGGLCY 60
 QY 61 NGVHEGGYQFVPIPLSPKNSYCGTQSEYKPPYHFSYHIVSNDTIVVKNQPNYSFS 120
 Db 61 NGVHEGGYQFVPIPLSPKNSYCGTQSEYKPPYHFSYHIVSNDTIVVKNQPNYSFS 120
 QY 121 CTYHSTYLVNQAFQQRVATVHVKNKSGMTFESQLSNFYTNNAKFSIKKEAPFVLEA 180
 Db 121 CTYHSTYLVNQAFQQRVATVHVKNKSGMTFESQLSNFYTNNAKFSIKKEAPFVLEA 180
 QY 181 GSDLFAGVEAKGLSIRFKVVLNSCWATPSADPMYPLQWLKNGCPTDETIVLVHNGRDH 240
 Db 181 GSDLFAGVEAKGLSIRFKVVLNSCWATPSADPMYPLQWLKNGCPTDETIVLVHNGRDH 240
 QY 241 RATFOFNAFRFONIPKLSKVLHCHETFCIDSEKLSCPVTCDKRLRLDQTGGVLVVELS 300
 Db 241 RATFOFNAFRFONIPKLSKVLHCHETFCIDSEKLSCPVTCDKRLRLDQTGGVLVVELS 300
 QY 301 LRSRGFSSLYSFDVLHLLIMLIGICAVL 329
 Db 301 LRSRGFSSLYSFDVLHLLIMLIGICAVL 329
 RESULT 6
 ADH48854
 ID ADH48854 standard; protein; 300 AA.
 XX
 AC ADH48854;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE NOV60A protein sequence, SEQ ID 138.
 XX
 KW Human; NOVX; atherosclerosis; hypertension; obesity; cancer; cytostatic;
 KW hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV60A;
 KW beta tectorin-like protein; chromosome 10.
 XX
 OS Homo sapiens.
 XX
 PN WO200268652-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 26-FEB-2002; 2002WO-0050910.
 XX
 PR 26-FEB-2001; 2001US-0271646P.
 PR 27-FEB-2001; 2001US-0271840P.
 PR 28-FEB-2001; 2001US-0272404P.
 PR 28-FEB-2001; 2001US-0272405P.
 PR 28-FEB-2001; 2001US-0272410P.
 PR 28-FEB-2001; 2001US-0272414P.
 PR 02-MAR-2001; 2001US-0272787P.
 PR 02-MAR-2001; 2001US-0272922P.
 PR 02-MAR-2001; 2001US-0273048P.
 PR 16-MAR-2001; 2001US-0273300P.
 PR 20-MAR-2001; 2001US-0276401P.
 PR 20-MAR-2001; 2001US-0277324P.

PR 20-MAR-2001; 2001US-0278660P.
 PR 30-MAR-2001; 2001US-0280039P.
 PR 30-MAR-2001; 2001US-0280234P.
 PR 02-APR-2001; 2001US-0280818P.
 PR 12-APR-2001; 2001US-0283443P.
 PR 23-APR-2001; 2001US-0285754P.
 PR 24-APR-2001; 2001US-0286096P.
 PR 03-MAY-2001; 2001US-0288353P.
 PR 17-MAY-2001; 2001US-0291703P.
 PR 31-MAY-2001; 2001US-0294834P.
 PR 20-JUN-2001; 2001US-0299695P.
 PR 21-JUN-2001; 2001US-0299845P.
 PR 05-JUL-2001; 2001US-0303242P.
 PR 13-AUG-2001; 2001US-0311981P.
 PR 16-AUG-2001; 2001US-0312858P.
 PR 17-AUG-2001; 2001US-0313280P.
 PR 29-AUG-2001; 2001US-0315614P.
 PR 17-SEP-2001; 2001US-0322818P.
 PR 25-FEB-2002; 2002US-00322818.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Alsobrook JP, Anderson DW, Ballinger RA, Boldog FL, Burgess CE;
 PI Casman SJ, Ellerman KE, Gangolli EA, Gerlach VL, Gilbert JA;
 PI Gorman L, Guo X, Gusev VV, Kekuda R, Li L, Liu X, Malyankar UM;
 PI Miller CE, Millet I, Padigar M, Patturajan M, Pena CEA, Peyman JA;
 PI Rastelli L, Shenoy SG, Shimkets RA, Smichson G, Spytek KA, Stone DJ;
 PI Taupier RJ, Tchernev VT, Vernet CAM, Zerhusen BD;
 XX
 XX WPI; 2002-698672/75.
 DR N-PSDB; ADH48853.
 XX
 PT New NOVX polypeptides or polynucleotides, useful for preventing or
 PT treating disorders or syndromes e.g., atherosclerosis, hypertension,
 PT obesity or cancer.
 PS
 PS Claim 1; Page 335; 923pp; English.
 XX
 CC The present invention relates to novel human NOVX proteins, where X is
 CC any number from 1 to 91 and their coding sequences. The proteins and
 CC coding sequences are useful for preventing or treating disorders or
 CC syndromes e.g. atherosclerosis, hypertension, obesity or cancer. NOV60 is
 CC a beta tectorin-like protein and its coding sequence maps to chromosome
 CC 10.
 XX
 SQ Sequence 300 AA;
 Query Match 87.7%; Score 1539.5; DB 5; Length 300;
 Best Local Similarity 89.4%; Pred. No. 4e-157;
 Matches 295; Conservative 2; Mismatches 2; Indels 31; Gaps 3;
 QY 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGVHQLALGGLCY 60
 Db 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGVHQLALGGLCY 60
 QY 61 NGVHEGGYQFVPIPLSPKNSYCGTQSEYKPPYHFSYHIVSNDTIVVKNQPNYSFS 120
 Db 61 NGVHEGGYQFVPIPLSPKNSYCGTQSEYKPPYHFSYHIVSNDTIVVKNQPNYSFS 120
 QY 121 CTYHSTYLVNQAFQQRVATVHVKNKSGMTFESQLSNFY-TNAKFSIKKEAPFVLEA 179
 Db 121 CTYHSTYLVNQAFQ-----SVNFLPKNAKFSIKKEAPFVLEA 161
 QY 180 IGSDLFAGVEAKGLSIRFKVVLNSCWATPSADPMYPLQWLKNGCPTDETIVLVHNGRD 239
 Db 162 IGSDLFAGVEAKGLSIRFKVVLNSCWATPSADPMYPLQWLKNGCPTDETIVLVHNGRD 221
 QY 240 HRATFOFNAFRFONIPKLSKVLHCHETFCIDSEKLSCPVTCDKRLRLDQTGGVLVVEL 299
 Db 222 HRATFOFNAFRFONIPKLSKVLHCHETFCIDSEKLSCPVTCDKRLRLDQTGGVLVVEL 281
 QY 300 LRSRGFSSLYSFDVLHLLIMLIGICAVL 329
 ||| :|||||

Db 282 SLR-----NVLHLLIMMLGICAVL 300

RESULT 7
ADH72160
ID ADH72160 standard; protein; 300 AA.
AC ADH72160;
XX
XX
DT 25-MAR-2004 (first entry)
XX
DE Human protein of the invention NOV48b SEQ ID NO:1056.
XX
KW human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.

PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403488P.
PR 13-AUG-2002; 2002US-0403499P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.

PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VV, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigarum M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Schiore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

WPI: 2004-081935/08.
N-PSDB; ADH72159.

New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

Example 48; SEQ ID NO 1056; 1880pp; English.

The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and anilipaeamic activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynucleotides comprising any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence represents a NOVX polypeptide of the invention.

SQ Sequence 300 AA;

Query Match 87.7%; Score 1539.5; DB 8; Length 300;
Best Local Similarity 89.4%; Pred. No. 4e-157;
Matches 295; Conservative 2; Mismatches 2; Indels 31; Gaps 3;

PS Example 48; SEQ ID NO 1060; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A

CC polypeptide of the invention has cytostatic, immunomodulator,

CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and

CC antilipemic activity, and may have a use in gene therapy, and as a

CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising

CC any of the 303 fully defined nucleotide sequences given in the

CC specification. The polypeptide is useful in the manufacture of a

CC medicament for treating a syndrome associated with a human disease. The

CC polypeptide, polynucleotide and antibody are useful in diagnosing,

CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,

CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are

CC further used as hybridisation probes, in chromosome mapping, tissue

CC typing, preventive medicine, and pharmacogenomics. The present sequence

CC represents a NOVX polypeptide of the invention.

XX

SQ Sequence 276 AA;

Query Match 85.7%; Score 1505; DB 8; Length 276;

Best Local Similarity 100.0%; Pred. No. 1.9e-153; Mismatches 0; Indels 0; Gaps 0;

Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 KSCAPKADVILVFCYKPTIITKIPECYGVWVHQLGGLCYNGVHEGGYQFVIPDLS 77

DB 1 KSCAPKADVILVFCYKPTIITKIPECYGVWVHQLGGLCYNGVHEGGYQFVIPDLS 60

QY 78 PKNKSYCGTQSYKPIHYFHYSHIVSNDTIVTKQPNVNSFSCYTHSYLVNQAAFDQR 137

DB 61 PKNKSYCGTQSYKPIHYFHYSHIVSNDTIVTKQPNVNSFSCYTHSYLVNQAAFDQR 120

QY 138 VATVHVKGSMGTFFESQSLNFTYTNAKFSIKKEAPFVLEASIGSDLFAGVEAKGLSIRF 197

DB 121 VATVHVKGSMGTFFESQSLNFTYTNAKFSIKKEAPFVLEASIGSDLFAGVEAKGLSIRF 180

QY 198 KVVLSNCWATPSADFMYPQLQWLNKGCPTDFTVLVHNGRDRHRTFQNAFRFQNIPLK 257

DB 181 KVVLSNCWATPSADFMYPQLQWLNKGCPTDFTVLVHNGRDRHRTFQNAFRFQNIPLK 240

QY 258 SKVWLHCETFFICDSKLSCPVTCDDKRLRLRDQTGG 293

DB 241 SKVWLHCETFFICDSKLSCPVTCDDKRLRLRDQTGG 276

RESULT 9

ADH72166

ID ADH72166 standard; protein; 273 AA.

AC ADH72166;

XX

DT 25-MAR-2004 (first entry)

XX

DE Human protein of the invention NOV48e SEQ ID NO:1062.

XX human; cytostatic; immunomodulator; neuroprotective; nootropic;

KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;

KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;

KW obesity; diabetes; infectious disease; metabolic syndrome X;

XX dyslipidaemia.

OS Homo sapiens.

XX

PN WO2003102155-A2.

XX

PD 11-DEC-2003.

XX

XX 03-JUN-2003; 2003WO-US017430.

XX

XX 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

XX

PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.

PR 06-JUN-2002; 2002US-0386864P.

PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

PR 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.

PR 07-JUN-2002; 2002US-0386942P.

PR 07-JUN-2002; 2002US-0386971P.

PR 07-JUN-2002; 2002US-0387262P.

PR 08-JUN-2002; 2002US-0296960P.

PR 10-JUN-2002; 2002US-0387400P.

PR 10-JUN-2002; 2002US-0387535P.

PR 11-JUN-2002; 2002US-0387610P.

PR 11-JUN-2002; 2002US-0387625P.

PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.

PR 11-JUN-2002; 2002US-0387696P.

PR 11-JUN-2002; 2002US-0387702P.

PR 11-JUN-2002; 2002US-0387836P.

PR 11-JUN-2002; 2002US-0387859P.

PR 12-JUN-2002; 2002US-0387933P.

PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.

PR 12-JUN-2002; 2002US-0388022P.

PR 12-JUN-2002; 2002US-0388096P.

PR 13-JUN-2002; 2002US-0389123P.

PR 14-JUN-2002; 2002US-0389118P.

PR 14-JUN-2002; 2002US-0389120P.

PR 14-JUN-2002; 2002US-0389144P.

PR 14-JUN-2002; 2002US-0389146P.

PR 17-JUN-2002; 2002US-0389729P.

PR 17-JUN-2002; 2002US-0389742P.

PR 18-JUN-2002; 2002US-0389844P.

PR 19-JUN-2002; 2002US-0390006P.

PR 19-JUN-2002; 2002US-0390209P.

PR 21-JUN-2002; 2002US-0390763P.

PR 17-JUL-2002; 2002US-0396706P.

PR 06-AUG-2002; 2002US-0401628P.

PR 09-AUG-2002; 2002US-0402156P.

PR 09-AUG-2002; 2002US-0402256P.

PR 09-AUG-2002; 2002US-0402389P.

PR 12-AUG-2002; 2002US-0402786P.

PR 12-AUG-2002; 2002US-0402816P.

PR 12-AUG-2002; 2002US-0402821P.

PR 12-AUG-2002; 2002US-0402832P.

PR 13-AUG-2002; 2002US-0403448P.

PR 13-AUG-2002; 2002US-0403531P.

PR 13-AUG-2002; 2002US-0403532P.

PR 13-AUG-2002; 2002US-0403563P.

PR 13-AUG-2002; 2002US-0406317P.

PR 15-AUG-2002; 2002US-0403617P.

PR 26-AUG-2002; 2002US-0406355P.

PR 26-AUG-2002; 2002US-0406240P.

PR 27-AUG-2002; 2002US-0406240P.

PR 12-SEP-2002; 2002US-0410084P.

PR 20-SEP-2002; 2002US-0412528P.

PR 23-SEP-2002; 2002US-0412731P.

PR 30-SEP-2002; 2002US-0414801P.

PR 30-SEP-2002; 2002US-0414839P.

PR 30-SEP-2002; 2002US-0414840P.

PR 30-SEP-2002; 2002US-0414954P.

PR 09-OCT-2002; 2002US-0417186P.

PR 09-OCT-2002; 2002US-0417406P.

PR 23-OCT-2002; 2002US-0420639P.

PR 28-OCT-2002; 2002US-0421156P.

PR 31-OCT-2002; 2002US-0422690P.

PR 01-NOV-2002; 2002US-0423130P.

PR 05-NOV-2002; 2002US-0423798P.

PR 05-NOV-2002; 2002US-0423798P.

PR 12-NOV-2002; 2002US-0425453P.

XX

Accession	Species	Location/Qualifiers	Sequence
KW	human	wild-type; diagnosis; renal disease; predisposition; medullary cystic kidney disease 2; MCKD2;	
KW	human	familial juvenile gouty nephropathy; FJGN; renal failure; hyperuricaemia;	
KW	human	gouty arthritis; enuresis.	
XX			
OS	Rattus norvegicus.		
XX			
PH	Key	Location/Qualifiers	
FT	Misc-difference 104	/note= "Position of missense mutation"	
FT	Misc-difference 149	/note= "Position of missense mutation"	
FT	Misc-difference 220	/note= "Position of missense mutation"	
FT	Misc-difference 220	/note= "Position of missense mutation"	
XX			
PN	WO2004038377-A2.		
XX			
PD	06-MAY-2004.		
XX			
PF	23-OCT-2003; 2003WO-US033957.		
XX			
PR	23-OCT-2002; 2002US-0420768P.		
PR	02-DEC-2002; 2002US-0430318P.		
XX			
PA	(UYPI-) UNIV PITTSBURGH.		
PA	(UYWA-) UNIV WAKE FOREST.		
XX			
PI	Hart TC, Hart PS, Gorry M, Bleyer AJ;		
XX			
DR	WPI; 2004-399985/37.		
DR	GENBANK; M63510.		
XX			
PT	Diagnosing renal diseases or a predisposition to renal diseases, e.g.		
PT	renal failure, hyperuricemia, gouty arthritis or enuresis comprises		
PT	assaying a genetic material to detect a mutation in at least a copy of		
PT	the uromodulin genetic sequence.		
XX			
PS	Disclosure; Fig 6; 24pp; English.		
XX			
CC	This sequence represents rat uromodulin (UMOD). The cDNA encoding this		
CC	sequence was used in the method of the invention for diagnosing a disease		
CC	or a predisposition to contract a disease. The method comprises obtaining		
CC	genetic material from a test subject and assaying the genetic material to		
CC	detect a mutation in at least a copy of the UMOD genetic sequence, where		
CC	the presence of a UMOD mutation supports a diagnosis of a disease or a		
CC	predisposition to contract a disease within the patient. The method also		
CC	comprises comparing the sequence of the genetic material of the sequence		
CC	of the wild-type UMOD gene and identifying any differences between the		
CC	sequence of the genetic material and the wild-type UMOD gene. The method		
CC	is useful for diagnosing renal diseases or a predisposition to renal		
CC	diseases, e.g. medullary cystic kidney disease 2 (MCKD2), familial		
CC	juvenile gouty nephropathy (FJGN), renal failure, hyperuricaemia, gouty		
CC	arthritis or enuresis.		
XX			
XX	Sequence 644 AA;		
XX			
XX	Query Match	13.0%; Score 228.5; DB 8; Length 644;	
XX	Best Local Similarity	27.3%; Pred. No. 6e-15;	
XX	Matches	57; Conservative 50; Mismatches 91; Indels 11; Gaps 7	
QY	76	LSPKNKSYCGTQSEYKPIYHYFISHVNSDITTVIKVQPNVYSFCTYHSTLVN-QAAF 134	
Db	384	VTTPARDGPGCTVLR-RNETHATYSNTLYLASEIIIRINIRINFECSYPLDMKVKSLKTSL 442	
QY	135	DORVATVHVKNSMGTFESQSLNPFYTNKAFSIKKEAPPVLEASIGSDLPFAGVEAKGLS 194	
Db	443	QPMVSAINLSLGGTGGKFTQMAL--FQNPFTYQPYQGPSWMLSTE--APLYVGTWLDGDD 498	
QY	195	I-RFKVNLNSCWATPSADPMYFLOWLKNGCP--TDETVLVHENGDRHRATFQFNARFF 251	
Db	499	LSRFVLLMTNCVATPSSNSTDPVKFIIQDRCPHTEDTTTIQTWENGSSQARFSIQMPFRF 558	
QY	252	QNIPKLSKWLHCFTFICDSEKSLCPVTC 280	

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 XX in gene mapping.
 PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
 XX selected from one of the 2722 sequences defined in the specification. A
 XX polynucleotide of the invention may have a use in gene therapy. The human
 XX diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 XX used to diagnose a particular condition, disease or disorder associated
 XX with human molecules, e.g. cell proliferative disorders,
 XX autoimmune/inflammatory disorder, developmental disorder, endocrine
 XX disorder, neurological disorders, gastrointestinal disorders, or
 XX infections caused by virus, bacteria, fungi or parasite. The dithp
 XX molecules may also be used in genetic mapping, in identifying individuals
 XX from minute biological samples, in detecting single nucleotide
 XX polymorphisms, as molecular weight markers, and for somatic or germline
 XX gene therapy. The present sequence represents a dithp protein of the
 XX invention. Note: The sequence data for this patent is not represented in
 XX the printed specification, but was obtained in electronic format directly
 XX from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX SQ Sequence 640 AA;

Query Match 12.6%; Score 221; DB 8; Length 640;
 Best Local Similarity 25.7%; Pred. No. 3.8e-14;
 Matches 66; Conservative 49; Mismatches 102; Indels 40; Gaps 9;
 QY 76 LSPKNSYCGTQSEYKPIYHFYSHIVSNDTIVVKNQPNVYFSCYTHSTYLVN-QAAF 134
 DB 381 VTPARDGPGTGMT-RNETHATYNTLYLADEIIIRDLNIRINACSYPLDMKVSLSKTL 439
 QY 135 DQVATVHVKNKSGMGTFFESQLS- - - - -NFYTNAPSIKKEAPVLEASIGSDLPAG 187
 DB 440 QPMVSALNIRVGTGTFVTRMALFQSPYTPQYQSSVTLSTEAFLYVGTMLDGGDL- - - 496
 QY 188 VEAKGLSIRFKVNLNSCWATPSADFMYPQLQINKGCP- - -TDETVLVHENGDRHRATFQ 245
 DB 497 - - - - -SRFALLMTNCTYATPSSNATDPLKYFIQDRCPHTRDSTIQVVENGESSQGRFS 549
 QY 246 FNAFRQNI PKLSKVWLHCETFCIDSEKLSCPVTCDKRLLRDOTGGVL- - -VVEL- - 299
 DB 550 VQMFRRFAG- - -NYDLVYLHCEVYLCDTMNEKCKPTCSG- - - - -TRFRSGSVIDQSRVNLNLP 603
 QY 300 - - - - -SLRSRGSFL 309
 DB 604 ITRKGQVATVSRAFSSL 620

XX

RESULT 15
 ID ADO59935 standard; protein; 643 AA.
 XX AC ADO59935;
 XX DT 29-JUL-2004 (first entry)
 XX DE Bovine UMOD.
 XX human; bovine; murine; rat; uromodulin; UMOD; assay; detection; mutation;
 KW wild-type; diagnosis; renal disease; predisposition;
 KW medullary cystic kidney disease 2; MCKD2;
 KW familial juvenile gouty nephropathy; FUGN; renal failure; hyperuricaemia;
 KW gouty arthritis; enuresis.
 XX OS Bos taurus.
 XX FH Key Location/Qualifiers
 FT Misc-difference 105 /note= "Position of missense mutation"
 FT Misc-difference 150 /note= "Position of missense mutation"
 FT Misc-difference 219 /note= "Position of missense mutation"

/note= "Position of missense mutation"

WO2004038377-A2.

06-MAY-2004.

23-OCT-2003; 2003WO-US033957.

23-OCT-2002; 2002US-0420768P.

02-DEC-2002; 2002US-0430318P.

(UYPI-) UNIV PITTSBURGH.

(UYWA-) UNIV WAKE FOREST.

Hart TC, Hart PS, Gorry M, Bleyer AJ;

WPI; 2004-399985/37.

GENBANK; S75958.

Diagnosing renal diseases or a predisposition to renal diseases, e.g.
 PT renal failure, hyperuricaemia, gouty arthritis or enuresis comprises
 PT assaying a genetic material to detect a mutation in at least a copy of
 PT the uromodulin genetic sequence.

Disclosure; Fig 6; 24pp; English.

PS This sequence represents bovine uromodulin (UMOD). The cDNA encoding this
 XX sequence was used in the method of the invention for diagnosing a disease
 XX or a predisposition to contract a disease. The method comprises obtaining
 XX genetic material from a test subject and assaying the genetic material to
 XX detect a mutation in at least a copy of the UMOD genetic sequence, where
 XX the presence of a UMOD mutation supports a diagnosis of a disease or a
 XX predisposition to contract a disease within the patient. The method also
 XX comprises comparing the sequence of the genetic material of the sequence
 XX of the wild-type UMOD gene and identifying any differences between the
 XX sequence of the genetic material and the wild-type UMOD gene. The method
 XX is useful for diagnosing renal diseases or a predisposition to renal
 XX diseases, e.g. medullary cystic kidney disease 2 (MCKD2), familial
 XX juvenile gouty nephropathy (FUGN), renal failure, hyperuricaemia, gouty
 XX arthritis or enuresis.

Sequence 643 AA;

Query Match 12.5%; Score 220; DB 8; Length 643;
 Best Local Similarity 25.8%; Pred. No. 4.9e-14;
 Matches 59; Conservative 46; Mismatches 98; Indels 26; Gaps 7;

QY 76 LSPKNSYCGTQSEYKPIYHFYSHIVSNDTIVVKNQPNVYFSCYTHSTYLVN-QAAF 134
 DB 383 VTPARDGPGTGMT-RNETHATYNTLYLADEIIIRDLNIRINACSYPLDMKVSLSKTL 441
 QY 135 DQVATVHVKNKSGMGTFFESQLS- - - - -NFYTNAPSIKKEAPVLEASIGSDLPAG 187
 DB 442 QPMVSALNIRVGTGTFVTRMALFQSPYTPQYQSSVTLSTEAFLYVGTMLDGGDL- - - 498
 QY 188 VEAKGLSIRFKVNLNSCWATPSADFMYPQLQINKGCP- - -TDETVLVHENGDRHRATFQ 245
 DB 499 - - - - -SRFVLLMTNCTYATPSSNATDPLKYFIQDRCPRAADSTIQVVENGESSQGRFS 551
 QY 246 FNAFRQNI PKLSKVWLHCETFCIDSEKLSCPVTCDK- - -RKRLRDOT 291
 DB 552 VQMFRRFAG- - -NYDLVYLHCEVYLCDTMNEKCKPTCPETFRSGSIIDOT 598

Search completed: July 20, 2005, 20:34:12
 Job time : 170 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:23:55 ; Search time 43 Seconds
(without alignments)
571.152 Million cell updates/sec

Title: US-10-687-268-35
Perfect score: 1756
Sequence: 1 MVTAKFVLIAIAFAEASAKSC.....YSFSDVHLHLMGICAVL 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
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5: /cgn2_6/prodata/1/iaa/PCUS COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	12.9	614	US-09-949-016-8536	Sequence 8536, Ap
2	213	12.1	380	US-09-949-016-8534	Sequence 8534, Ap
3	213	12.1	380	US-09-949-016-8535	Sequence 8535, Ap
4	210	12.0	530	US-09-949-016-6085	Sequence 6085, Ap
5	210	12.0	554	US-09-949-016-8532	Sequence 8532, Ap
6	210	12.0	554	US-09-949-016-8533	Sequence 8533, Ap
7	210	12.0	554	US-09-949-016-9420	Sequence 9420, Ap
8	210	12.0	554	US-09-949-016-9421	Sequence 9421, Ap
9	209	11.9	384	US-08-350-435-2	Sequence 2, Appli
10	209	11.9	384	US-09-15916-2	Sequence 2, Appli
11	172	9.8	607	US-09-907-794A-190	Sequence 190, App
12	172	9.8	607	US-09-905-125A-190	Sequence 190, App
13	172	9.8	607	US-09-902-775A-190	Sequence 190, App
14	172	9.8	607	US-09-906-701A-190	Sequence 190, App
15	172	9.8	607	US-09-903-603A-190	Sequence 190, App
16	172	9.8	607	US-09-904-920A-190	Sequence 190, App
17	172	9.8	607	US-09-909-064A-190	Sequence 190, App
18	172	9.8	607	US-09-905-381A-190	Sequence 190, App
19	172	9.8	607	US-09-906-618-190	Sequence 190, App
20	155	8.8	254	US-09-808-701A-30	Sequence 30, Appl
21	150.5	8.6	1785	US-09-341-587-3	Sequence 3, Appli
22	149	8.5	545	US-10-067-422-11	Sequence 11, Appl
23	148.5	8.5	566	US-08-484-993B-41	Sequence 41, Appl
24	148.5	8.5	566	US-08-484-158B-41	Sequence 41, Appl
25	148.5	8.5	566	US-08-484-596A-41	Sequence 41, Appl
26	148.5	8.5	566	US-08-480-150A-41	Sequence 41, Appl
27	148.5	8.5	566	US-08-458-731-41	Sequence 41, Appl

28	148.5	8.5	566	3	US-08-149-223A-41	Sequence 41, Appl
29	148.5	8.5	713	2	US-08-484-993B-2	Sequence 2, Appli
30	148.5	8.5	713	2	US-08-484-158B-2	Sequence 2, Appli
31	148.5	8.5	713	2	US-08-484-596A-2	Sequence 2, Appli
32	148.5	8.5	713	2	US-08-480-150A-2	Sequence 2, Appli
33	148.5	8.5	713	3	US-08-149-223A-2	Sequence 2, Appli
34	148.5	8.5	713	3	US-08-458-731-2	Sequence 2, Appli
35	147.5	8.4	1290	1	US-08-470-350B-2	Sequence 2, Appli
36	144	8.2	713	1	US-08-453-472-6	Sequence 6, Appli
37	144	8.2	713	1	US-08-038-948-7	Sequence 7, Appli
38	144	8.2	713	1	US-08-038-948-8	Sequence 8, Appli
39	144	8.2	713	1	US-08-038-948-10	Sequence 10, Appl
40	144	8.2	713	1	US-08-453-952-6	Sequence 6, Appli
41	144	8.2	713	2	US-08-862-903-6	Sequence 6, Appli
42	142	8.1	716	2	US-08-484-993B-14	Sequence 14, Appl
43	142	8.1	716	2	US-08-484-158B-14	Sequence 14, Appl
44	142	8.1	716	2	US-08-484-596A-14	Sequence 14, Appl
45	142	8.1	716	2	US-08-480-150A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-8536
; Sequence 8536, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8536
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8536

Query Match	12.9%	Score 227;	DB 4;	Length 614;
Best Local Similarity	24.3%	Pred. No. 1.4e-15;		
Matches	81;	Conservative 55;	Mismatches 127;	Indels 70; Gaps 14;
QY	13	ABASAKCAPNKADVLVFCYPKTIITIKIPCEPYGWEVHQLAGLCYN-GVHEGGYYQF 71		
Db	296	ASVQVKACAGG-----YVYNLTAPPECHLAYCTDPSSVEGTCECSIDE----- 340		
QY	72	VIPDLSPKN-KSYCG-----TOSEYKP-----PIYHPYSHIVNDTIVVKNQPVNYSF 119		
Db	341	--DCKSNNGRWHCCQCKQDFNITAPHKPGPRNETHATYSNTLYLADSIIRDLNINFIN 397		
QY	120	SCYTHSTYLVN-QAADFQVATVHVXGSMCTFESQLSL-----NFTYNAKFSIKKEA 171		
Db	398	ACSPFLDMKSLKTLQPMWSALNIRVGCTGNFTVRNALFOTPSYQYQSSVTLSTEA 457		
QY	172	PFVLEASBISGDLFAGVEAKGLSIRFKVVLNSCWATPSADPMYPLQWLINKGCP--TDE 229		
Db	458	FLYVGTMLDGGDL-----SRFALLMTCVATPSSNATDPLKYFIIDRCFPHTRDS 507		
QY	230	TVLVHENGDRIRATFQFNAPFRQNIPLKSLVHLHCETIFCDSEKLSCEVTCCKRLLRD 289		
Db	508	TIQVENGESSQGRFSVQMERFAG--NYDLVYLHCEVYLCDTMNEKCKPTCSG----TRF 561		
QY	290	QTGGVL----VVEL-----SLSRSGFSSL 309		

Db 265 WSVTSPVQASACRNIL-RNQTALYKNTLSLVNDFFIIRDTILNINFCAYPLDMKVS 323
QY 131 QAAFDQVATVHVKNMGSMGTFSQSL--NFYTNAKFSIKKEAPFVLEASIG--SDLF 185
Db 324 QAAQPIVSSLNVSDGNGEFIVRMALFDQNTN-----PYEGDAVELSVESVLY 374
QY 186 AG-VEAKGLSIRPKVVLNSCWATPSADFMYPQLWLNKGCPT--DETVLVHENGDRHRA 242
Db 375 VGAILEQDTSRFLNLCYATPTEDKADLVKYFIIRNSCSNQRDSTIHVEENGQSSS 434
QY 243 TQFNARFQNIPLSKVWLHCETFCIDSEKLSCPVTCCK 282
Db 435 RFSVQMFAGHYDL--VFLHCEIHLCDLSLNEQCQPCSCSR 472

RESULT 5
US-09-949-016-8532
; Sequence 8532, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8532
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8532

Query Match 12.0%; Score 210; DB 4; Length 554;
Best Local Similarity 26.8%; Pred. No. 8.4e-14;
Matches 75; Conservative 43; Mismatches 104; Indels 59; Gaps 11;

QY 32 CYPKTIITKIPCEPYGWEVHQLAGGLCYNGHGGYQFVIPDL----- 76
Db 246 CGPREIKVKVDC-----LLGGL-----GLGEEVIAYLRDPNCSSILOTEERN 288

QY 77 -----SPKNKSYCGTQSEVKPPIYHFYSHVSNDDTTIVIKNOPVNSFSCVHSTYLVN- 130
Db 289 WSVTSPVQASACRNIL-RNQTALYKNTLSLVNDFFIIRDTILNINFCAYPLDMKVS 347

QY 131 QAAFDQVATVHVKNMGSMGTFSQSL--NFYTNAKFSIKKEAPFVLEASIG--SDLF 185
Db 348 QAAQPIVSSLNVSDGNGEFIVRMALFDQNTN-----PYEGDAVELSVESVLY 398

QY 186 AG-VEAKGLSIRPKVVLNSCWATPSADFMYPQLWLNKGCPT--DETVLVHENGDRHRA 242
Db 399 VGAILEQDTSRFLNLCYATPTEDKADLVKYFIIRNSCSNQRDSTIHVEENGQSSS 458

QY 243 TQFNARFQNIPLSKVWLHCETFCIDSEKLSCPVTCCK 282
Db 459 RFSVQMFAGHYDL--VFLHCEIHLCDLSLNEQCQPCSCSR 496

RESULT 6
US-09-949-016-8533
; Sequence 8533, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8533
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8533

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8533
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8533

Query Match 12.0%; Score 210; DB 4; Length 554;
Best Local Similarity 26.8%; Pred. No. 8.4e-14;
Matches 75; Conservative 43; Mismatches 104; Indels 59; Gaps 11;

QY 32 CYPKTIITKIPCEPYGWEVHQLAGGLCYNGHGGYQFVIPDL----- 76
Db 246 CGPREIKVKVDC-----LLGGL-----GLGEEVIAYLRDPNCSSILOTEERN 288

QY 77 -----SPKNKSYCGTQSEVKPPIYHFYSHVSNDDTTIVIKNOPVNSFSCVHSTYLVN- 130
Db 289 WSVTSPVQASACRNIL-RNQTALYKNTLSLVNDFFIIRDTILNINFCAYPLDMKVS 347

QY 131 QAAFDQVATVHVKNMGSMGTFSQSL--NFYTNAKFSIKKEAPFVLEASIG--SDLF 185
Db 348 QAAQPIVSSLNVSDGNGEFIVRMALFDQNTN-----PYEGDAVELSVESVLY 398

QY 186 AG-VEAKGLSIRPKVVLNSCWATPSADFMYPQLWLNKGCPT--DETVLVHENGDRHRA 242
Db 399 VGAILEQDTSRFLNLCYATPTEDKADLVKYFIIRNSCSNQRDSTIHVEENGQSSS 458

QY 243 TQFNARFQNIPLSKVWLHCETFCIDSEKLSCPVTCCK 282
Db 459 RFSVQMFAGHYDL--VFLHCEIHLCDLSLNEQCQPCSCSR 496

RESULT 7
US-09-949-016-9420
; Sequence 9420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9420
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9420

Query Match 12.0%; Score 210; DB 4; Length 554;
Best Local Similarity 26.8%; Pred. No. 8.4e-14;
Matches 75; Conservative 43; Mismatches 104; Indels 58; Gaps 11;

QY 32 CYPKTIITKIPCEPYGWEVHQLAGGLCYNGHGGYQFVIPDL----- 76

Db	246	CGPREIKVKVDKC-----LJLGL-----GLGEVIAYLRDPCNSSILOTEERN	288
Qy	77	-----SPKNKSYCGTQSEYKPPYIHFYSHIVSNDTTVIKQNPVNYFSCTYHSTYLVN-	130
Db	289	WVSVTSPVQASACRNILE-RNQTHAIYKNTLSLVNDFIIRDITILNFOCAPLDMKVSL	347
Qy	131	QAAPFORVATVHVKNKSGMTTFESQLSL---NFYTNAKSIKKEAPVLEASIG--SDLF	185
Db	348	QAALQPIVSSNLVSDVNGGEFTVRNALFDQQNTN-----PYEGDAVELSVESVLY	398
Qy	186	AG-VEAKGLSRFRKVVNLSCWATPSPADFMYPLOWOLINKGCPT--DETVLVHENGDRHRA	242
Db	399	VGAILEQGDTSRFLNVLRCNATPTEDKADLVKVFILNRSCNQDSTIHVEENGQSSS	458
Qy	243	TFQNAFRQNPQIPKLSKVLWLCETTFICDSEKLSCPVTCDK	282
Db	459	RFSVQMFMFAGHYDL--VFLHCEIHLCDSLNEQCQPCSCR	496
RESULT 8			
US-09-949-016-9421			
; Sequence 9421, Application US/09949016			
; Patent No. 6812339			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF			
; FILE REFERENCE: CL001307			
; CURRENT APPLICATION NUMBER: US/09/949,016			
; CURRENT FILING DATE: 2000-04-14			
; PRIOR APPLICATION NUMBER: 60/241,755			
; PRIOR FILING DATE: 2000-10-20			
; PRIOR APPLICATION NUMBER: 60/237,768			
; PRIOR FILING DATE: 2000-10-03			
; PRIOR APPLICATION NUMBER: 60/231,498			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 207012			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 9421			
; LENGTH: 554			
; TYPE: PRT			
; ORGANISM: Human			
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Query Match		12.0%;	Score 210; DB 4; Length 554;
Best Local Similarity		26.8%;	Pred. No. 8.4e-14;
Matches		75; Conservative	43; Mismatches 104; Indels 58; Gaps 11;
Qy	32	CYPKTIITIKIEPCPGVEVHQIALGGLCVNGVHEGGYQFVTPDL-----	76
Db	246	CGPREIKVKVDKC-----LJLGL-----GLGEVIAYLRDPCNSSILOTEERN	288
Qy	77	-----SPKNKSYCGTQSEYKPPYIHFYSHIVSNDTTVIKQNPVNYFSCTYHSTYLVN-	130
Db	289	WVSVTSPVQASACRNILE-RNQTHAIYKNTLSLVNDFIIRDITILNFOCAPLDMKVSL	347
Qy	131	QAAPFORVATVHVKNKSGMTTFESQLSL---NFYTNAKSIKKEAPVLEASIG--SDLF	185
Db	348	QAALQPIVSSNLVSDVNGGEFTVRNALFDQQNTN-----PYEGDAVELSVESVLY	398
Qy	186	AG-VEAKGLSRFRKVVNLSCWATPSPADFMYPLOWOLINKGCPT--DETVLVHENGDRHRA	242
Db	399	VGAILEQGDTSRFLNVLRCNATPTEDKADLVKVFILNRSCNQDSTIHVEENGQSSS	458
Qy	243	TFQNAFRQNPQIPKLSKVLWLCETTFICDSEKLSCPVTCDK	282
Db	459	RFSVQMFMFAGHYDL--VFLHCEIHLCDSLNEQCQPCSCR	496

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; Patent No. 563315
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; GENERAL INFORMATION:
; APPLICANT: Scheele, George
; APPLICANT: Fukuoka, Shin-Ichi
; TITLE OF INVENTION: GP2 and Diagnosis of
; TITLE OF INVENTION: Pancreatitis
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,435
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06184/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 384 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-350-435-2
;
Query Match 11.9%; Score 209; DB 1;
Best Local Similarity 24.8%; Pred. No. 6.2e-14;
Matches 98; Conservative 49; Mismatches 116;

QY 1 MVTAKFVLIA----IPAASA-----KS
DB 1 MVGGGLLWLLALNSCILTOASAVQRDPDPTVEDKKCEKA
QY 23 --NKADV---ILVFCVPKTIITKIPECVPGVEVHQLALG
DB 61 DLMSSDVHSLQPDQCGPREIKVKDKC-----LQG
QY 77 -----SPKNKSYCGTQSEYKPIYH
DB 104 RDPNCSSIIQLTEERNWVSVTPVQASACRNILE-RNQTHA
QY 117 YPSCTYHSTLYLN-QAAFDQRVATVHVKNKSGMGTFESQI
DB 163 INFQCAPYLDMKVSLQAALQPIVSSLNVDGNGEFIVRM
QY 173 FVLEASEIG--SOLFAG-VEAKGLSRFRKVLNLSNCWATPS
DB 214 YEGDAVELSVESVLYVGAILEQGDTSRFNLVLENCYATPTPT
QY 228 DETVLVHNGRDRHRTQFNARFRQNIPLKSKVLHLCETFE
DB 274 DSTIHVENGQSSESRFSVQMFMFAGHYDL--VFLFCEIH

RESULT 10
PCT-US95-15916-2
; Sequence 2, Application PC/TUS9515916
; GENERAL INFORMATION:
; APPLICANT: ALPHAGENE, INC.
; TITLE OF INVENTION: Diagnosis of Pancreatitis

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Db 264 SIYAENINTSLTSSDRMRVLSKSYL-----AFNS--NG 298
Qy 67 GYQFVLPDLSPKNSY-----CGTQSEYKPPYHVFYSHIV-----SNDTTVIVKQ 113
Db 299 NNQLQKPTCPKLSNVVFSVPLNGCGTIRKVEDQSI--TYTNIITFSASSTSEVITRQK 357
Qy 114 PWNYSFCT--YHSTYLVNQAFQDQVATVHVYKNGSMGTFFESQSLNFTVNAKFSIKKEA 171
Db 358 QLIIVKCEMGNSTVEIYITDDVIQS-----QNALGKNTSMAL--FESNSFEKTILES 412
Qy 172 PFVLEASIGSLDFAGVEAKGLSIRFKVVLNSCWATPSADFMYPQLQWLNKGCPTDVT 231
Db 413 PYVY---DLNQLTFVQVSLHTSDPNLVFLDTCRASPTSDPASP--TYDLIKSGCSRDTC 468
Qy 232 LVHENGDRHRATFQNAFRFQNIPLKSKVWLHCETFIQDS--EKUSCPVTCDKRRK 285
Db 469 KYVPL-FGHYGRFQFNAFKF--LRSMSSVYLQCKVLICDSSDHQSRQNCQGVSRSK 521

RESULT 12
US-09-905-125A-190
; Sequence 190, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 190
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-190

Query Match 9.8%; Score 172; DB 4; Length 607;
Best Local Similarity 23.3%; Pred. No. 1.3e-09;
Matches 69; Conservative 54; Mismatches 115; Indels 58; Gaps 14;

Qy 10 AIPAE---ASAKSCAPNKADVILVFCYPKTIITKIPECPYGVHQLALGCLCYNGVHEG 66
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Qy 67 GYQFVLPDLSPKNSY-----CGTQSEYKPPYHVFYSHIV-----SNDTTVIVKQ 113
Db 299 NNQLQKPTCPKLSNVVFSVPLNGCGTIRKVEDQSI--TYTNIITFSASSTSEVITRQK 357
Qy 114 PWNYSFCT--YHSTYLVNQAFQDQVATVHVYKNGSMGTFFESQSLNFTVNAKFSIKKEA 171
Db 358 QLIIVKCEMGNSTVEIYITDDVIQS-----QNALGKNTSMAL--FESNSFEKTILES 412
Qy 172 PFVLEASIGSLDFAGVEAKGLSIRFKVVLNSCWATPSADFMYPQLQWLNKGCPTDVT 231
Db 413 PYVY---DLNQLTFVQVSLHTSDPNLVFLDTCRASPTSDPASP--TYDLIKSGCSRDTC 468
Qy 232 LVHENGDRHRATFQNAFRFQNIPLKSKVWLHCETFIQDS--EKUSCPVTCDKRRK 285
Db 469 KYVPL-FGHYGRFQFNAFKF--LRSMSSVYLQCKVLICDSSDHQSRQNCQGVSRSK 521

RESULT 13
US-09-902-775A-190
; Sequence 190, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann


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; LENGTH: 607
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-700-190

Query Match          9.8%; Score 172; DB 4; Length 607;
Best Local Similarity 23.3%; Pred. No. 1.3e-09;
Matches 69; Conservative 54; Mismatches 115; Indels 58; Gaps 14;

QY 10 AIFAE---ASAKCAPNKADVILVFCYKPTIITKIPECPYGVHQLALGGLCYNGVHEG 66
Db 264 SIYAENINTSLTSSDRMRVLSKSYLE-----AFNS--NG 298

QY 67 GYQFVIPDLSPKNKSY-----CCTQSEYKPPYHYFYSHIV-----SNDTTVIVKQ 113
Db 299 NNLLQKOPTCRPKLSNVVFEVPLNGCGTIRKVEDQSI--TYNIIITFSASSTSEVITRQK 357

QY 114 PVNYSFSC--YHSTYLVNQAAFDQVATVHVKNGSMGTFFESQLSLNFTYNAKFSIKKEA 171
Db 358 QLOIIVKCEMGNSTVEIYITDDVIOQ-----QNALGKYNTSMAL-FESNSFEKTILES 412

QY 172 PFVLEASIGSLFAGVEAKGLSIRFKVLNSCWATPSADPMYPLQWOLINKGCPDDET 231
Db 413 PYV---DLNQTLFQVLSLHSDPNLVFLDTCRASPTSDFASP--TYDLIKSGGSRDTC 468

QY 232 LVHENGDRHRATFOFNAPFRQNIPLKSKVWLHCETFFICDS--EKLSCPVTCDKRRK 285
Db 469 KYVPL-FGHYGRFQFNAKFF--LRSMSSVYLQCKVLICDSDHQSRQCGVSRSK 521
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RESULT 15

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US-09-903-603A-190
; Sequence 190, Application US/0903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, David
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
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; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 190
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-603A-190

Query Match          9.8%; Score 172; DB 4; Length 607;
Best Local Similarity 23.3%; Pred. No. 1.3e-09;
Matches 69; Conservative 54; Mismatches 115; Indels 58; Gaps 14;

QY 10 AIFAE---ASAKCAPNKADVILVFCYKPTIITKIPECPYGVHQLALGGLCYNGVHEG 66
Db 264 SIYAENINTSLTSSDRMRVLSKSYLE-----AFNS--NG 298

QY 67 GYQFVIPDLSPKNKSY-----CCTQSEYKPPYHYFYSHIV-----SNDTTVIVKQ 113
Db 299 NNLLQKOPTCRPKLSNVVFEVPLNGCGTIRKVEDQSI--TYNIIITFSASSTSEVITRQK 357

QY 114 PVNYSFSC--YHSTYLVNQAAFDQVATVHVKNGSMGTFFESQLSLNFTYNAKFSIKKEA 171
Db 358 QLOIIVKCEMGNSTVEIYITDDVIOQ-----QNALGKYNTSMAL-FESNSFEKTILES 412

QY 172 PFVLEASIGSLFAGVEAKGLSIRFKVLNSCWATPSADPMYPLQWOLINKGCPDDET 231
Db 413 PYV---DLNQTLFQVLSLHSDPNLVFLDTCRASPTSDFASP--TYDLIKSGGSRDTC 468

QY 232 LVHENGDRHRATFOFNAPFRQNIPLKSKVWLHCETFFICDS--EKLSCPVTCDKRRK 285
Db 469 KYVPL-FGHYGRFQFNAKFF--LRSMSSVYLQCKVLICDSDHQSRQCGVSRSK 521
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Search completed: July 20, 2005, 20:37:54
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:31:30 ; Search time 157 Seconds
(without alignments)
813.464 Million cell updates/sec

Title: US-10-687-268-35

Perfect score: 1756

Sequence: 1 MVTRAFVLLAFAEASAKS.....YFSDVHLHMLGICAVL 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1736639 seqs, 388189149 residues

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1756	100.0	329 15	US-10-312-088-35
2	1756	100.0	329 15	US-10-085-198-142
3	1756	100.0	329 18	US-10-687-268-35
4	1751	99.7	329 15	US-10-085-198-140
5	1665	94.8	329 18	US-10-687-268-46
6	1539.5	87.7	300 15	US-10-085-198-138
7	219	12.5	577 15	US-10-108-260A-3485
8	219	12.5	673 15	US-10-104-047-2774
9	213	12.1	406 9	US-09-925-297-726
10	210	12.0	530 9	US-09-872-153-17
11	210	12.0	534 17	US-10-485-555-52

12	174	9.9	620	15	US-10-187-975-110	Sequence 110, App
13	173.5	9.9	1011	15	US-10-161-493-136	Sequence 136, App
14	172	9.8	530	15	US-10-330-051A-70	Sequence 70, Appl
15	172	9.8	585	9	US-09-864-711-14	Sequence 14, Appl
16	172	9.8	607	9	US-09-909-320-190	Sequence 190, App
17	172	9.8	607	9	US-09-909-088B-190	Sequence 190, App
18	172	9.8	607	9	US-09-905-291A-190	Sequence 190, App
19	172	9.8	607	9	US-09-902-853-190	Sequence 190, App
20	172	9.8	607	9	US-09-907-824-190	Sequence 190, App
21	172	9.8	607	9	US-09-907-841-190	Sequence 190, App
22	172	9.8	607	10	US-09-904-011-190	Sequence 190, App
23	172	9.8	607	10	US-09-903-640-190	Sequence 190, App
24	172	9.8	607	10	US-09-908-093-190	Sequence 190, App
25	172	9.8	607	10	US-09-906-742-190	Sequence 190, App
26	172	9.8	607	10	US-09-906-838-190	Sequence 190, App
27	172	9.8	607	10	US-09-907-813-190	Sequence 190, App
28	172	9.8	607	10	US-09-907-942-190	Sequence 190, App
29	172	9.8	607	10	US-09-904-859-190	Sequence 190, App
30	172	9.8	607	10	US-09-909-204-190	Sequence 190, App
31	172	9.8	607	10	US-09-904-820-190	Sequence 190, App
32	172	9.8	607	10	US-09-904-786-190	Sequence 190, App
33	172	9.8	607	10	US-09-906-646-190	Sequence 190, App
34	172	9.8	607	10	US-09-906-700-190	Sequence 190, App
35	172	9.8	607	10	US-09-903-786-190	Sequence 190, App
36	172	9.8	607	10	US-09-902-903-190	Sequence 190, App
37	172	9.8	607	10	US-09-903-749A-190	Sequence 190, App
38	172	9.8	607	10	US-09-904-119-190	Sequence 190, App
39	172	9.8	607	10	US-09-904-956-190	Sequence 190, App
40	172	9.8	607	10	US-09-902-736-190	Sequence 190, App
41	172	9.8	607	10	US-09-907-794-190	Sequence 190, App
42	172	9.8	607	10	US-09-903-943-190	Sequence 190, App
43	172	9.8	607	10	US-09-904-462-190	Sequence 190, App
44	172	9.8	607	10	US-09-907-925-190	Sequence 190, App
45	172	9.8	607	10	US-09-902-692-190	Sequence 190, App

ALIGNMENTS

RESULT 1
US-10-312-088-35
; Sequence 35, Application US/10312088
; Publication No. US20030219862A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Cogswell, John P.
; APPLICANT: Kabnic, Karen S.
; APPLICANT: Lai, Ying-Ta
; APPLICANT: Martensen, Shelby A.
; APPLICANT: Murock, Paul R.
; APPLICANT: Smith, Randall F.
; APPLICANT: Strum, Jay C.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Rizni, Safia K.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50029
; CURRENT APPLICATION NUMBER: US/10/312,088
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/19929
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,161
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/213,156
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-312-088-35

Query Match 100.0%; Score 1756; DB 15; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.9e-175; Indels 0; Gaps 0;
Matches 329; Conservative 0; Mismatches 0;

Qy 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKTIITKIPECPYGWEVHQLALGGLCY 60
Db 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKTIITKIPECPYGWEVHQLALGGLCY 60

Qy 61 NGVHEGGYYQFVLPDLSPKNKSYCGTQSEYKPPYIHFYSHIVSNDTTVIVKNQPNYSFS 120
Db 61 NGVHEGGYYQFVLPDLSPKNKSYCGTQSEYKPPYIHFYSHIVSNDTTVIVKNQPNYSFS 120

Qy 121 CTYHSTYLVNQAAFDQVRVATVHVKNKSGMTFESQSLNFTYNAKFSIKKEAPFVLESEI 180
Db 121 CTYHSTYLVNQAAFDQVRVATVHVKNKSGMTFESQSLNFTYNAKFSIKKEAPFVLESEI 180

Qy 181 GSDLFAGVEAKGLSIRFKVNLNSCWATPSADFMYPLOWQLINKGCPDTDETIVLHENGDRH 240
Db 181 GSDLFAGVEAKGLSIRFKVNLNSCWATPSADFMYPLOWQLINKGCPDTDETIVLHENGDRH 240

Qy 241 RATFOFNAFRFQNIPLSKVWLHCETFCIDSEKLSCPVTCDKRKLRLRDQGGVVLVVELS 300
Db 241 RATFOFNAFRFQNIPLSKVWLHCETFCIDSEKLSCPVTCDKRKLRLRDQGGVVLVVELS 300

Qy 301 LRSRGFSSLSYFSFSDVLHLLIMMLGICAVL 329
Db 301 LRSRGFSSLSYFSFSDVLHLLIMMLGICAVL 329

RESULT 2

US-10-085-198-142
; Sequence 142, Application US/10085198
; Publication No. US2004000907A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-142

Query Match 100.0%; Score 1756; DB 15; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.9e-175; Indels 0; Gaps 0;
Matches 329; Conservative 0; Mismatches 0;

Qy 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKTIITKIPECPYGWEVHQLALGGLCY 60

Db 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKTIITKIPECPYGWEVHQLALGGLCY 60

Qy 61 NGVHEGGYYQFVLPDLSPKNKSYCGTQSEYKPPYIHFYSHIVSNDTTVIVKNQPNYSFS 120
Db 61 NGVHEGGYYQFVLPDLSPKNKSYCGTQSEYKPPYIHFYSHIVSNDTTVIVKNQPNYSFS 120

Qy 121 CTYHSTYLVNQAAFDQVRVATVHVKNKSGMTFESQSLNFTYNAKFSIKKEAPFVLESEI 180
Db 121 CTYHSTYLVNQAAFDQVRVATVHVKNKSGMTFESQSLNFTYNAKFSIKKEAPFVLESEI 180

Qy 181 GSDLFAGVEAKGLSIRFKVNLNSCWATPSADFMYPLOWQLINKGCPDTDETIVLHENGDRH 240
Db 181 GSDLFAGVEAKGLSIRFKVNLNSCWATPSADFMYPLOWQLINKGCPDTDETIVLHENGDRH 240

Qy 241 RATFOFNAFRFQNIPLSKVWLHCETFCIDSEKLSCPVTCDKRKLRLRDQGGVVLVVELS 300
Db 241 RATFOFNAFRFQNIPLSKVWLHCETFCIDSEKLSCPVTCDKRKLRLRDQGGVVLVVELS 300

Qy 301 LRSRGFSSLSYFSFSDVLHLLIMMLGICAVL 329
Db 301 LRSRGFSSLSYFSFSDVLHLLIMMLGICAVL 329

RESULT 3
US-10-687-268-35
; Sequence 35, Application US/10687268
; Publication No. US20050137129A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Lee, Judithann M.
; APPLICANT: Smith, Randall F.
; APPLICANT: White, John R.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50029-1
; CURRENT APPLICATION NUMBER: US/10/687,268
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/213,161
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/213,156
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US01/19929
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 10/312,088
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-687-268-35

Query Match 100.0%; Score 1756; DB 18; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.9e-175; Indels 0; Gaps 0;
Matches 329; Conservative 0; Mismatches 0;

Qy 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKTIITKIPECPYGWEVHQLALGGLCY 60
Db 1 MVTAFVLLAIFAEASAKSCAPNKADVLVFCYPTKTIITKIPECPYGWEVHQLALGGLCY 60

Qy 61 NGVHEGGYYQFVLPDLSPKNKSYCGTQSEYKPPYIHFYSHIVSNDTTVIVKNQPNYSFS 120
Db 61 NGVHEGGYYQFVLPDLSPKNKSYCGTQSEYKPPYIHFYSHIVSNDTTVIVKNQPNYSFS 120

Qy 121 CTYHSTYLVNQAAFDQVRVATVHVKNKSGMTFESQSLNFTYNAKFSIKKEAPFVLESEI 180
Db 121 CTYHSTYLVNQAAFDQVRVATVHVKNKSGMTFESQSLNFTYNAKFSIKKEAPFVLESEI 180

Qy 181 GSDLFAGVEAKGLSIRFKVNLNSCWATPSADFMYPLOWQLINKGCPDTDETIVLHENGDRH 240
Db 181 GSDLFAGVEAKGLSIRFKVNLNSCWATPSADFMYPLOWQLINKGCPDTDETIVLHENGDRH 240

QY 241 RATFOFNAFRFONIPKLSKVWLHCETFCDSKLSCPVTCDKRKLRLRDQTGGVLVVELS 300
Db |||||
241 RATFOFNAFRFONIPKLSKVWLHCETFCDSKLSCPVTCDKRKLRLRDQTGGVLVVELS 300
QY 301 LRSRGFSSLSYFSDVLHLLIMLIGICAVL 329
Db |||||
301 LRSRGFSSLSYFSDVLHLLIMLIGICAVL 329

RESULT 4
US-10-085-198-140
; Sequence 140, Application US/10085198
; Publication No. US2004000907A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 140
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-140

Query Match 99.7%; Score 1751; DB 15; Length 329;
Best Local Similarity 99.7%; Pred. No. 6.3e-175;
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MVTAFVLLAIPAEASAKSCAPNKADVLVFCYKPTIITKIPECYGVWEVHQLAGGLCY 60
Db 1 MVTAFVLLAIPAEASAKSCAPNKADVLVFCYKPTIITKIPECYGVWEVHQLAGGLCY 60
QY 61 NGVHEGGYQFVPIPLSPKNSYCGTQSEYKPPYHFSYHIVSNDDTVIVKQPNYSFS 120
Db 61 NGVHEGGYQFVPIPLSPKNSYCGTQSEYKPPYHFSYHIVSNDDTVIVKQPNYSFS 120
QY 121 CTYHSTYLVNQAFDQFVATVHVKNKSGMTFESQSLNFTYNNAKFSIKKEAPFVLEAISEI 180
Db 121 CTYHSTYLVNQAFDQFVATVHVKNKSGMTFESQSLNFTYNNAKFSIKKEAPFVLEAISEI 180
QY 181 GSDLFAGVEAKGLSRFKVNLNSCWATPSADPMYPLQMLINKGCTPTDVLVHENGDRH 240
Db 181 GSDLFAGVEAKGLSRFKVNLNSCWATPSADPMYPLQMLINKGCTPTDVLVHENGDRH 240
QY 241 RATFOFNAFRFONIPKLSKVWLHCETFCDSKLSCPVTCDKRKLRLRDQTGGVLVVELS 300
Db 241 RATFOFNAFRFONIPKLSKVWLHCETFCDSKLSCPVTCDKRKLRLRDQTGGVLVVELS 300
QY 301 LRSRGFSSLSYFSDVLHLLIMLIGICAVL 329

RESULT 5
US-10-687-268-46
; Sequence 46, Application US/10687268
; Publication No. US20050137129A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Bankaj
; APPLICANT: Lee, Judithann M.
; APPLICANT: Smith, Randall F.
; APPLICANT: White, John R.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50029-1
; CURRENT APPLICATION NUMBER: US/10/687,268
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/213,161
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/213,156
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US01/19929
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 10/312,088
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-687-268-46

Query Match 94.8%; Score 1665; DB 18; Length 329;
Best Local Similarity 94.2%; Pred. No. 6.9e-166;
Matches 310; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
QY 1 MVTAFVLLAIPAEASAKSCAPNKADVLVFCYKPTIITKIPECYGVWEVHQLAGGLCY 60
Db 1 MVTAFVLLAIPAEASAKSCAPNKADVLVFCYKPTIITKIPECYGVWEVHQLAGGLCY 60
QY 61 NGVHEGGYQFVPIPLSPKNSYCGTQSEYKPPYHFSYHIVSNDDTVIVKQPNYSFS 120
Db 61 NGVHEGGYQFVPIPLSPKNSYCGTQSEYKPPYHFSYHIVSNDDTVIVKQPNYSFS 120
QY 121 CTYHSTYLVNQAFDQFVATVHVKNKSGMTFESQSLNFTYNNAKFSIKKEAPFVLEAISEI 180
Db 121 CTYHSTYLVNQAFDQFVATVHVKNKSGMTFESQSLNFTYNNAKFSIKKEAPFVLEAISEI 180
QY 181 GSDLFAGVEAKGLSRFKVNLNSCWATPSADPMYPLQMLINKGCTPTDVLVHENGDRH 240
Db 181 GSDLFAGVEAKGLSRFKVNLNSCWATPSADPMYPLQMLINKGCTPTDVLVHENGDRH 240
QY 241 RATFOFNAFRFONIPKLSKVWLHCETFCDSKLSCPVTCDKRKLRLRDQTGGVLVVELS 300
Db 241 RATFOFNAFRFONIPKLSKVWLHCETFCDSKLSCPVTCDKRKLRLRDQTGGVLVVELS 300
QY 301 LRSRGFSSLSYFSDVLHLLIMLIGICAVL 329
Db 301 LRSRGFSSLSYFSDVLHLLIMLIGICAVL 329

RESULT 6
US-10-085-198-138
; Sequence 138, Application US/10085198
; Publication No. US2004000907A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646

Query Match 99.7%; Score 1751; DB 15; Length 329;
Best Local Similarity 99.7%; Pred. No. 6.3e-175;
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MVTAFVLLAIPAEASAKSCAPNKADVLVFCYKPTIITKIPECYGVWEVHQLAGGLCY 60
Db 1 MVTAFVLLAIPAEASAKSCAPNKADVLVFCYKPTIITKIPECYGVWEVHQLAGGLCY 60
QY 61 NGVHEGGYQFVPIPLSPKNSYCGTQSEYKPPYHFSYHIVSNDDTVIVKQPNYSFS 120
Db 61 NGVHEGGYQFVPIPLSPKNSYCGTQSEYKPPYHFSYHIVSNDDTVIVKQPNYSFS 120
QY 121 CTYHSTYLVNQAFDQFVATVHVKNKSGMTFESQSLNFTYNNAKFSIKKEAPFVLEAISEI 180
Db 121 CTYHSTYLVNQAFDQFVATVHVKNKSGMTFESQSLNFTYNNAKFSIKKEAPFVLEAISEI 180
QY 181 GSDLFAGVEAKGLSRFKVNLNSCWATPSADPMYPLQMLINKGCTPTDVLVHENGDRH 240
Db 181 GSDLFAGVEAKGLSRFKVNLNSCWATPSADPMYPLQMLINKGCTPTDVLVHENGDRH 240
QY 241 RATFOFNAFRFONIPKLSKVWLHCETFCDSKLSCPVTCDKRKLRLRDQTGGVLVVELS 300
Db 241 RATFOFNAFRFONIPKLSKVWLHCETFCDSKLSCPVTCDKRKLRLRDQTGGVLVVELS 300
QY 301 LRSRGFSSLSYFSDVLHLLIMLIGICAVL 329

Query Match 94.8%; Score 1665; DB 18; Length 329;
Best Local Similarity 94.2%; Pred. No. 6.9e-166;
Matches 310; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
QY 1 MVTAFVLLAIPAEASAKSCAPNKADVLVFCYKPTIITKIPECYGVWEVHQLAGGLCY 60
Db 1 MVTAFVLLAIPAEASAKSCAPNKADVLVFCYKPTIITKIPECYGVWEVHQLAGGLCY 60
QY 61 NGVHEGGYQFVPIPLSPKNSYCGTQSEYKPPYHFSYHIVSNDDTVIVKQPNYSFS 120
Db 61 NGVHEGGYQFVPIPLSPKNSYCGTQSEYKPPYHFSYHIVSNDDTVIVKQPNYSFS 120
QY 121 CTYHSTYLVNQAFDQFVATVHVKNKSGMTFESQSLNFTYNNAKFSIKKEAPFVLEAISEI 180
Db 121 CTYHSTYLVNQAFDQFVATVHVKNKSGMTFESQSLNFTYNNAKFSIKKEAPFVLEAISEI 180
QY 181 GSDLFAGVEAKGLSRFKVNLNSCWATPSADPMYPLQMLINKGCTPTDVLVHENGDRH 240
Db 181 GSDLFAGVEAKGLSRFKVNLNSCWATPSADPMYPLQMLINKGCTPTDVLVHENGDRH 240
QY 241 RATFOFNAFRFONIPKLSKVWLHCETFCDSKLSCPVTCDKRKLRLRDQTGGVLVVELS 300
Db 241 RATFOFNAFRFONIPKLSKVWLHCETFCDSKLSCPVTCDKRKLRLRDQTGGVLVVELS 300
QY 301 LRSRGFSSLSYFSDVLHLLIMLIGICAVL 329
Db 301 LRSRGFSSLSYFSDVLHLLIMLIGICAVL 329

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; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 138
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-138

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Query Match      87.7%; Score 1539.5; DB 15; Length 300;
Best Local Similarity 89.4%; Pred. No. 9.2e-153;
Matches 295; Conservative 2; Mismatches 2; Indels 31; Gaps 3;

QY 1 MYTAFVLLAFAEASAKAPNADVILFCYKPTIITKIPECPYGEVHQLALGGLCY 60
DB 1 MYTAFVLLAFAEASAKAPNADVILFCYKPTIITKIPECPYGEVHQLALGGLCY 60

QY 61 NGVHEGGYQFVPIPLSPKNSYCTQSEYKPPPIYHSHVNSDNTTVIVKQPNVYFS 120
DB 61 NGVHEGGYQFVPIPLSPKNSYCTQSEYKPPPIYHSHVNSDNTTVIVKQPNVYFS 120

QY 121 CYTHSTYLVNQAFQDQVATVHVKNMGTPESQLSLNFY-TNAKFSIKKEAPFVLEAS 179
DB 121 CYTHSTYLVNQAFQDQVATVHVKNMGTPESQLSLNFY-TNAKFSIKKEAPFVLEAS 161

QY 180 IGSDFAGVEAKGLSIRFKVNLNSCWATPSADFMYPLOWQLINKGCPDTEVTVHENG 239
DB 162 IGSDFAGVEAKGLSIRFKVNLNSCWATPSADFMYPLOWQLINKGCPDTEVTVHENG 221

QY 240 HRATQFNAFRONTIPKLSKVLHCEVTCIDSEKLSCPVTCCKRKLRLDQGTGGVVL 299
DB 222 HRATQFNAFRONTIPKLSKVLHCEVTCIDSEKLSCPVTCCKRKLRLDQGTGGVVL 281

QY 300 SLRSRGFSSLSYFSDVHLHLMGLICAVL 329
DB 282 SLR-----NVLHLMGLICAVL 300

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```

RESULT 7
US-10-108-260A-3485
; Sequence 3485, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3485
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-10-108-260A-3485

```

Query Match      12.5%; Score 219; DB 15; Length 577;
Best Local Similarity 25.7%; Pred. No. 1.3e-13;
Matches 66; Conservative 49; Mismatches 102; Indels 40; Gaps 9;

QY 76 LSPKNSYCGTQSEYKPPPIYHSHVNSDNTTVIVKQPNVYFSCTYHSTYLVN-QAAF 134
DB 318 VTPARDGPGCTVLT-RNETHATYNTLYLADEIIIRDNLINIKINFACSYPLDMKVS 376
QY 135 DQVATVHVKNMGTPESQLSL-----NFYTNAKFSIKKEAPFVLEASIGSDLFAG 187
DB 377 QPMVSALNIRVGGTGMFTVRMALTQPSYTOPYQSSVTLSTEAFVLTMDGGDL--- 433
QY 188 VEAKGLSIRFKVNLNSCWATPSADFMYPLOWQLINKGCP--TDETIVLVHENG 245
DB 434 -----SRFALLMNTCYATPSSNATDPLKYFIIDRCPTHTRDSTIQVVENGE 486
QY 246 FNAFRQNIPLKSKVLHCEVTCIDSEKLSCPVTCCKRKLRLDQGTGGVVL---V 299
DB 487 VQMFRRFAG--NYDLVYLHCEVYLCDTNEKCKPTCSG-----TRFRSGSV 540
QY 300 -----SLRSRGFSSL 309
DB 541 ITRKGQVATVSRAFSSL 557

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RESULT 8

```

US-10-104-047-2774
; Sequence 2774, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2774
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2774

```

```

Query Match      12.5%; Score 219; DB 15; Length 673;
Best Local Similarity 25.7%; Pred. No. 1.6e-13;
Matches 66; Conservative 49; Mismatches 102; Indels 40; Gaps 9;

QY 76 LSPKNSYCGTQSEYKPPPIYHSHVNSDNTTVIVKQPNVYFSCTYHSTYLVN-QAAF 134
DB 414 VTPARDGPGCTVLT-RNETHATYNTLYLADEIIIRDNLINIKINFACSYPLDMKVS 472
QY 135 DQVATVHVKNMGTPESQLSL-----NFYTNAKFSIKKEAPFVLEASIGSDLFAG 187
DB 473 QPMVSALNIRVGGTGMFTVRMALTQPSYTOPYQSSVTLSTEAFVLTMDGGDL--- 529
QY 188 VEAKGLSIRFKVNLNSCWATPSADFMYPLOWQLINKGCP--TDETIVLVHENG 245
DB 530 -----SRFALLMNTCYATPSSNATDPLKYFIIDRCPTHTRDSTIQVVENGE 582
QY 246 FNAFRQNIPLKSKVLHCEVTCIDSEKLSCPVTCCKRKLRLDQGTGGVVL---V 299
DB 583 VQMFRRFAG--NYDLVYLHCEVYLCDTNEKCKPTCSG-----TRFRSGSV 636
QY 300 -----SLRSRGFSSL 309
DB 637 ITRKGQVATVSRAFSSL 653

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RESULT 9

```

US-09-925-297-726
; Sequence 726, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 726
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (160)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-726

Query Match
Best Local Similarity 12.1%; Score 213; DB 9; Length 406;
Matches 89; Conservative 48; Mismatches 116; Indels 98; Gaps 15;

QY 1 MYTKAFVLLA-----KSCAP-----NK 24
DB 27 MVGSLGLWALSCILTOASAVQRPSTVEDCEKACRPEEBECALALNSTWGCFCRQDLNS 86
QY 25 ADV-----ILVFCYKTIITKIPCEPYGWEVHQLGGLCYNGVHEGGYQFVIPDL----- 76
DB 87 SDVHSLQPLDQCPREIKVKDKC-----LLGGL-----GLGEVIAYLRDPN 129
QY 77 -----SPKNKSYCGTQSEYKPIYHYFHYSHIVNSDNTTVIVKQPNVNSPS 120
DB 130 CSSILOTEERNVSVTPVQASACRNILE-RNQTTHAIYKNTLSLVNDFIIRTNINQ 188
QY 121 CTHSTYLVN-QAADFQVRVATVHVKNVSGMTFESQLSL----NFYTNKFSIKKEAPFVLE 176
DB 189 CAYPLDMKVSQAALQPIVSSLSNVSDGNGEFIVRMALFQDQNYTN-----PYEGD 239
QY 177 ASEIG--SDFPAG-VEAKGLSRFKVVLNSCWATPSADPMYPLQWLKNGCPT--DET 231
DB 240 AVESVSVLYVGAILEQDTSRFLNLCVATPTEDKADLVKYFIIRNSCSNQRDSTI 299
QY 232 LVHENGDRHRATFQFNAPRFQNIPLSKVWLHCETFCIDSEKLSCPVTCDK 282
DB 300 HVENGGQSSSRFSVQMFAGHYDL--VFLHCEIHLCDLSNEQCQPCSR 348

RESULT 10
US-09-872-153-17
; Sequence 17, Application US/09872153
; Patent No. US20020082207A1
; GENERAL INFORMATION:
; APPLICANT: First, Shannon K.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Dillon, David C.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.531
; CURRENT APPLICATION NUMBER: US/09/872,153
; CURRENT FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 530
; TYPE: PRT

Query Match
Best Local Similarity 12.0%; Score 210; DB 17; Length 534;
Matches 75; Conservative 43; Mismatches 104; Indels 58; Gaps 11;

QY 32 CYPKTIITKIPCEPYGWEVHQLGGLCYNGVHEGGYQFVIPDL----- 76
DB 226 CGPREIKVKDKC-----LLGGL-----GLGEVIAYLRDPNCSILQTEERN 268
QY 77 -----SPKNKSYCGTQSEYKPIYHYFHYSHIVNSDNTTVIVKQPNVNSPSCTHYSTYLVN- 130
DB 269 WWSVTSPVQASACRNILE-RNQTTHAIYKNTLSLVNDFIIRTNINQFQAYPLDMKVS 327
QY 131 QAAFQVRVATVHVKNVSGMTFESQLSL----NFYTNKFSIKKEAPFVLEASIG--SDF 185
DB 328 QAALQPIVSSLSNVSDGNGEFIVRMALFQDQNYTN-----PYEGDAVELSVESVLY 378
QY 186 AG-VEAKGLSRFKVVLNSCWATPSADPMYPLQWLKNGCPT--DET 242
DB 379 VGAILEQDTSRFLNLCVATPTEDKADLVKYFIIRNSCSNQRDSTI 438
QY 243 TFQFNAPRFQNIPLSKVWLHCETFCIDSEKLSCPVTCDK 282
DB 439 RFSVQMFAGHYDL--VFLHCEIHLCDLSNEQCQPCSR 476

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; ORGANISM: Homo sapien
US-09-872-153-17

Query Match
Best Local Similarity 12.0%; Score 210; DB 9; Length 530;
Matches 75; Conservative 43; Mismatches 104; Indels 58; Gaps 11;

QY 32 CYPKTIITKIPCEPYGWEVHQLGGLCYNGVHEGGYQFVIPDL----- 76
DB 222 CGPREIKVKDKC-----LLGGL-----GLGEVIAYLRDPNCSILQTEERN 264
QY 77 -----SPKNKSYCGTQSEYKPIYHYFHYSHIVNSDNTTVIVKQPNVNSPSCTHYSTYLVN- 130
DB 265 WWSVTSPVQASACRNILE-RNQTTHAIYKNTLSLVNDFIIRTNINQFQAYPLDMKVS 323
QY 131 QAAFQVRVATVHVKNVSGMTFESQLSL----NFYTNKFSIKKEAPFVLEASIG--SDF 185
DB 324 QAALQPIVSSLSNVSDGNGEFIVRMALFQDQNYTN-----PYEGDAVELSVESVLY 374
QY 186 AG-VEAKGLSRFKVVLNSCWATPSADPMYPLQWLKNGCPT--DET 242
DB 375 VGAILEQDTSRFLNLCVATPTEDKADLVKYFIIRNSCSNQRDSTI 434
QY 243 TFQFNAPRFQNIPLSKVWLHCETFCIDSEKLSCPVTCDK 282
DB 435 RFSVQMFAGHYDL--VFLHCEIHLCDLSNEQCQPCSR 472

RESULT 11
US-10-485-555-52
; Sequence 52, Application US/10485555
; Publication No. US20050120393A1
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc.
; TITLE OF INVENTION: Full Length Prostate Specific Polynucleotides and Polypeptides
; FILE REFERENCE: 9U 101.2 PCT
; CURRENT APPLICATION NUMBER: US/10/485,555
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,470
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/330,747
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-555-52

Query Match
Best Local Similarity 12.0%; Score 210; DB 17; Length 534;
Matches 75; Conservative 43; Mismatches 104; Indels 58; Gaps 11;

QY 32 CYPKTIITKIPCEPYGWEVHQLGGLCYNGVHEGGYQFVIPDL----- 76
DB 226 CGPREIKVKDKC-----LLGGL-----GLGEVIAYLRDPNCSILQTEERN 268
QY 77 -----SPKNKSYCGTQSEYKPIYHYFHYSHIVNSDNTTVIVKQPNVNSPSCTHYSTYLVN- 130
DB 269 WWSVTSPVQASACRNILE-RNQTTHAIYKNTLSLVNDFIIRTNINQFQAYPLDMKVS 327
QY 131 QAAFQVRVATVHVKNVSGMTFESQLSL----NFYTNKFSIKKEAPFVLEASIG--SDF 185
DB 328 QAALQPIVSSLSNVSDGNGEFIVRMALFQDQNYTN-----PYEGDAVELSVESVLY 378
QY 186 AG-VEAKGLSRFKVVLNSCWATPSADPMYPLQWLKNGCPT--DET 242
DB 379 VGAILEQDTSRFLNLCVATPTEDKADLVKYFIIRNSCSNQRDSTI 438
QY 243 TFQFNAPRFQNIPLSKVWLHCETFCIDSEKLSCPVTCDK 282
DB 439 RFSVQMFAGHYDL--VFLHCEIHLCDLSNEQCQPCSR 476

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:29:15 ; Search time 42 Seconds
(without alignments)
753.698 Million cell updates/sec

Title: US-10-687-268-35
Perfect score: 1756
Sequence: 1 MVTKAFVLLAIPAEASAKSC.....YSFSDVLHLLHMLGICAVL 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1357.5	77.3	329	A57246	beta-tectorin prec
2	230	13.1	2155	T30197	alpha tectorin - m
3	228.5	13.0	644	A40212	uromodulin precurs
4	228.5	13.0	644	I84634	Tamm-Horsfall prot
5	222.5	12.7	642	S52111	uromodulin precurs
6	220	12.5	530	A38690	membrane glycoprot
7	219	12.5	640	A30452	uromodulin precurs
8	210	12.0	509	A37259	membrane glycoprot
9	210	12.0	530	G02091	pancreatic zymogen
10	204	11.6	2120	T30243	alpha tectorin - c
11	150.5	8.6	2083	T43721	CRP-ductin-alpha p
12	150.5	8.6	2403	A59386	sanko - human
13	148.5	8.5	540	S70403	zona pellucida gly
14	148.5	8.5	713	S70434	zona pellucida gly
15	147.5	8.4	1290	A57190	ebnerin precursor
16	147.5	8.4	1594	T30549	hensin - rabbit
17	144	8.2	713	A34782	sperm-binding gly
18	142	8.1	716	S70398	zona pellucida gly
19	134	7.6	745	A48833	sperm-binding gly
20	133	7.6	570	S70400	zona pellucida gly
21	130.5	7.4	715	S70397	zona pellucida gly
22	130	7.4	540	A39783	sperm-binding gly
23	120.5	6.9	841	I50428	transforming growt
24	117	6.7	536	S35712	sperm-binding gly
25	113.5	6.5	676	A45984	sperm-binding gly
26	111.5	6.3	918	TJC361	scavenger receptor
27	99	5.6	928	1VGBEMC	glycoprotein B pre
28	94	5.4	423	F86313	F2H15.8 protein -
29	94	5.4	1086	T43266	DNA-directed DNA p

30	94	5.4	1086	2	T40242	DNA polymerase del
31	92	5.2	853	1	A41220	transforming growt
32	91.5	5.2	887	2	A54832	villin homolog qua
33	90.5	5.2	1280	2	A39117	170K lectin precu
34	89.5	5.1	653	2	G96675	hypothetical prote
35	89.5	5.1	693	2	T19551	mucin-like protein
36	88.5	5.0	317	2	G59103	hypothetical prote
37	88.5	5.0	478	2	T02629	vacuolar processin
38	88.5	5.0	1084	1	S19661	DNA-directed DNA p
39	88.5	5.0	1292	2	T09229	galactose binding
40	88	5.0	698	2	H71535	hypothetical prote
41	87.5	5.0	399	2	D96717	hypothetical prote
42	87.5	5.0	400	2	T51953	H-protein promoter
43	87.5	5.0	837	2	A42112	mucin-like peptide
44	87	5.0	623	2	I46382	ZP1 precursor - mo
45	86.5	4.9	440	2	T24323	hypothetical prote

ALIGNMENTS

RESULT 1

A57246
beta-tectorin precursor - chicken
C:Species: Gallus gallus (Chicken)
C>Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: A57246
R:Killick, R.; Legan, P.K.; Malenczak, C.; Richardson, G.P.
J. Cell Biol. 129, 535-547, 1995
A:Title: Molecular cloning of chick beta-tectorin, an extracellular matrix molecule of
A:Reference number: A57246; MUID:95238547; PMID:7721949
A:Accession: A57246
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-329 <KIL>
A:Cross-references: UNIPROT:P54097; GB:L38519; NID:G602439; PIDN:AAA92461.1; PID:G602440
C:Keywords: extracellular matrix; membrane protein; phosphatidylinositol linkage

Query Match 77.3%; Score 1357.5; DB 2; Length 329;
Best Local Similarity 73.6%; Pred. No. 4.9e-109;
Matches 242; Conservative 44; Mismatches 42; Indels 1; Gaps 1;

QY	1	MVTKAFVLLAIPAEASAKSCAPNKADVLVLCYCPKTIITKIPECPYGEVHQLALGLCY	60
DB	1	MVATVILMVLTAQAFAGCTPNKADVLVLCYPTIITKIPECPYGEVHQLALGLCY	60
QY	61	NGVHEGGYQFVLPDLSPNKSYCGTQSEYKPIYHFYSHIVSNDTTVIVKNQPVNYGFS	120
DB	61	NGIHDSGYYQFTIPDLSPNKSYCGTQSEKPNPVHYFNSIVSNDSTVIVKSQPVNYGFT	120
QY	121	CTYHSTVLVNOAADFQVATVHVKNSGMTFESQLSLNFTYNAKPSIKKEAPFVLEASEI	180
DB	121	CTYNANYLVNOAADFQVATVHVKNSGSGSPESQLSLNFTYNAKPSIKKEAPFVLEASEI	180
QY	181	GSDLFAGVEAKGLSRFRKVLNLSWATPSADFMPLQWLNKGCPTDETVLVHENGDRH	240
DB	181	GSDIFAGVEAKGLSDRFKVLNLSWATPSADFMPLQWLNKGCPTDETVLVHENGDRH	240
QY	241	RATQFNAPFQNTPKLSKWLHCETFTICDSEKLSCPVTCDKRKLRLDQGGVLVAVELS	300
DB	241	RATQFNAPFQNTPKLSKWLHCETFTICDSEKLSCPVTCDKRKLRLDQGGVLVAVELS	300
QY	301	LRSGFSSLSYFSDVLHLLHMLGICAVL	329
DB	300	VRNKGLSRFVMSDVIFHLLFAIGFCAIL	328

RESULT 2

T30197
alpha tectorin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30197

F:335-584/Domain: ZP domain homology <ZPH>

Query Match 12.7%; Score 222.5; DB 1; Length 642;
Best Local Similarity 26.3%; Pred. No. 4.3e-11;
Matches 55; Conservative 50; Mismatches 93; Indels 11; Gaps 7;

QY 76 LSPKNSYCGTQSEYKPIYHYSHIVSDTTIVKQNPVNSFCTYHSTYLVN-QAAF 134
DB 382 VTPARNGPCGTVLK-RNETHATYSTNTLYLANAIIIRIMNFECYPLDMKVSLSKTS 440
QY 135 DQVATVHVKNMGTFESQSLNFTYNAKPSIKKEAPVLEASIGSLDFAGVEAKGLS 194
DB 441 QPMVSLNLSLGGTGFVRLMAL--FQSPYTPQYQGPSVMLSTE--AFLYVGTMLDGGD 496

QY 195 I-RFKVVLNSCWATPSADPMYPLQWOLINKGCP--TDETVLVHNGRDHRAVTFQFNAPRF 251
DB 497 LSRFVLLMNCVATPSNSSTDVVKYFIQDSCPRTEDTIQVTEGSSQARFSVQMFRF 556
QY 252 QNPKLSKVLHCETFCIDSEKLSCPVTC 280
DB 557 AG--NYDLVYLHCVEVYLCDSSTGEQCKPTC 583

RESULT 6

A38690
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A38690; S11503; PNO573
R:Hoops, T.C.; Rindler, M.J.
J. Biol. Chem. 266, 4257-4263, 1991
A:Title: Isolation of the cDNA encoding glycoprotein-2 (GP-2), the major zymogen granule
A:Reference number: A38690; MUID:91154223; PMID:1999417
A:Accession: A38690
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <HO>
A:Cross-references: UNIPROT:P19218; GB:M58716; NID:G204453; PIDN:AAA41268.1; PID:G204454
R:Fukuoka, S.I.; Scheele, G.
Nucleic Acids Res. 18, 5900, 1990
A:Title: Nucleotide sequence encoding the major glycoprotein (GP2) of rat pancreatic sec
A:Reference number: S11503; MUID:91016950; PMID:2216794
A:Accession: S11503
A:Molecule type: DNA
A:Residues: 1-286, 'Q' 288-376, 'A' 378-530 <FUK>
A:Cross-references: EMBL:X53935; NID:G57246; PIDN:CAA37882.1; PID:G57247
R:Withiam-Leitch, M.; Aletta, J.M.; Koshlukova, S.E.; Rupp, G.; Beaudoin, A.R.; Rubin, R
Biochem. Biophys. Res. Commun. 194, 1167-1174, 1993
A:Title: Glycoprotein 2 of zymogen granule membranes shares immunological cross-reactivi
A:Reference number: PNO573; MUID:93356784; PMID:8352773
A:Accession: PNO573
A:Molecule type: protein
A:Residues: 327-376, 'A' 378-512 <WIT>
A:Experimental source: pancreas
C:Comment: This protein is a major protein of rat pancreatic zymogen granule membranes,
C:Superfamily: membrane glycoprotein 2; membrane glycoprotein 2 homology; ZP domain hom
C:Keywords: calcium binding; glycoprotein; lipoprotein; membrane protein; pancreas; phos
F:52-530/Domain: membrane glycoprotein 2 homology <MGH>
F:221-471/Domain: ZP domain homology <ZPH>
F:350,366,367,378/Binding site: phospholipid (Leu) #status predicted
F:375,377,397,420/Binding site: calcium (Val, Val, Thr, Asp) #status predicted

Query Match 12.5%; Score 220; DB 1; Length 530;
Best Local Similarity 27.1%; Pred. No. 5.5e-11;
Matches 78; Conservative 46; Mismatches 108; Indels 56; Gaps 12;

QY 23 NKADVI---LVFCYPKTIITKIPECYGVHQLAGGLCYNVHGGYGVFVLPDLS 78
DB 209 NVSDTLSQLDCCGNAEYKVLKDKC-----LLGGL-----GFKEDIITYLND 251
QY 79 KNSYVC-GTQSEYKPIYHYSHIVSD-----TTIVKQNPVN 116
DB 252 RN---CRGTMKDEPNWVSTTSPVANDCGNLENGTHAIYRNTLSLATDPIRDLVN 308

QY 117 YSFCTYHSTYLVN-QAAFQDQVATVHVKNMGTFESQSLNFTYNAKPSIKKEAPFVL 175
DB 309 VNFQCAVPLDMVNSLQALQPIVSSLVNDVVGAGEFTVTMAL--FQDQSYTHPYEGSKVL 366
QY 176 EASEIGSGLDFAGVEA-KGLSIRFKVVLNSCWATPSADPMYPLQWOLINKGCP--DET 232
DB 367 LPVE--NLTLYGVLLNRGDTSRFLKLLTNCVATPSGDRNDIVKVFIRNRCPNQDSTIN 424
QY 233 VHEGDRHRAVTFQFNAPRFQNIPLKLSKVLHCETFCIDSEKLSCPVTC 280
DB 425 VEENGVSSESRSFVQMFRPAG--NYDLVYLHCVEVYLCDSSTGEQCPSC 470

RESULT 7

A30452
uromodulin precursor - human
N:Alternate names: Tamm-Horsfall urinary glycoprotein; uromucoid
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A30452; A30453
R:Pennica, D.; Kohr, W.J.; Kuang, W.J.; Glaister, D.; Aggarwal, B.B.; Chen, E.Y.; Goede
Science 236, 83-88, 1987
A:Title: Identification of human uromodulin as the Tamm-Horsfall urinary glycoprotein.
A:Reference number: A30452; MUID:87177970; PMID:3453112
A:Accession: A30452
A:Molecule type: DNA; mRNA
A:Residues: 1-640 <PEN>
A:Cross-references: UNIPROT:P07911; GB:M15881; NID:G340163; PIDN:AAA36798.1; PID:G340164
A:Note: parts of this sequence, including the amino end of the mature protein, were dete
R:Heslin, C.; Decker, J.M.; Sherblom, A.P.; Kumar, S.; Yue, C.C.; Mattaliano, R.J.; Tiza
Science 237, 1479-1484, 1987
A:Title: Uromodulin (Tamm-Horsfall glycoprotein): A renal ligand for lymphokines.
A:Reference number: A30453; MUID:87319675; PMID:3498215
A:Accession: A30453
A:Molecule type: mRNA
A:Residues: 1-640 <HES>
A:Cross-references: GB:M17778
A:Note: the authors translated the codon GTG for residue 381 as Asp
A:Note: parts of this sequence, including the amino end of the mature protein, were dete
R:Rindler, M.J.; Naik, S.S.; Li, N.; Hoops, T.C.; Peraidi, M.N.
J. Biol. Chem. 265, 20784-20789, 1990
A:Title: Uromodulin (Tamm-Horsfall Glycoprotein/Uromucoid) is a phosphatidylinositol-lin
A:Reference number: A30454; MUID:91065873; PMID:2249987
A:Contents: annotation; GPI-anchor
C:Comment: The protein is anchored to the cell membrane by a phosphatidylinositol linkag
C:Genetics:
A:Gene: GDB:UMOD
A:Cross-references: GDB:133729; OMIM:191845
A:Map position: 16p13.11-16p12.3
A:Introns: 30/1; 289/1; 325/1; 394/3; 444/2; 526/2; 580/3; 608/1; 621/1
A:Note: the first intron occurs before the initiator codon
C:Superfamily: uromodulin; EGF homology; membrane glycoprotein 2 homology; ZP domain hom
C:Keywords: duplication; glycoprotein; lipoprotein; membrane protein; phosphatidylinosit
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-640/Product: uromodulin #status predicted <MAT>
F:69-106/Domain: EGF homology <EGF>
F:170-639/Domain: membrane glycoprotein 2 homology <MGH>
F:334-583/Domain: ZP domain homology <ZPH>
F:38,76,80,275,322,513/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:232,396/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 12.5%; Score 219; DB 1; Length 640;
Best Local Similarity 25.7%; Pred. No. 8.5e-11;
Matches 66; Conservative 49; Mismatches 102; Indels 40; Gaps 9;

QY 76 LSPKNSYCGTQSEYKPIYHYSHIVSDTTIVKQNPVNSFCTYHSTYLVN-QAAF 134
DB 381 VTPARNGPCGTVLK-RNETHATYSTNTLYLANAIIIRDLNINFACTYPLDMKVSLSK 439
QY 135 DQVATVHVKNMGTFESQSL-----NFTYNAKPSIKKEAPFVLEASIGSLD 187

Db 440 QPMVSALNIRVGGTGMFTVRMALFQTPSYTQPYQSGSVTLSTEAPLYVGTMLDGDGL--- 496

Qy 188 VEAKGLSIRFKVNLNSCWATPSADPMYPLQWLKNGCP--TDTVLVHNGRDHRAFPQ 245

Db 497 -----SRFALLMTCVATSSNATPLKFIQDRCPHTRDSTIQVENGSSQGRFS 549

Qy 246 FNAERFQNIPLSKVWLHCETFCIDSEKLSCPVTCDEKRLLRDQGTGVL-----VVEL-- 299

Db 550 VQMFRRFAG--NYDLVYLHCEVYLCDTMNEKCKPTCSG-----TRFRSGSVIDQSRVNLNLP 603

Qy 300 -----SLRSGRFSSL 309

Db 604 ITRKGQVATSRATSSSL 620

RESULT 8

membrane glycoprotein 2 precursor - dog

N:Alternate names: zymogen granule membrane associated protein ZAP75

C:Species: Canis lupus familiaris (dog)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A37259; PC2195

R:Fukuoka, S.I.; Freedman, S.D.; Scheele, G.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 2898-2902, 1991

A:Title: A single gene encodes membrane-bound and free forms of GP-2, the major glycoprotein of zymogen granules in the dog

A:Reference number: A37259; MUID:91187898; PMID:2011597

A:Accession: A37259

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-509 <FUK>

A:Cross-references: UNIPROT:P25291; GB:M64083; GB:M37032; NID:g164102; PIDN:AAA30904.1; R:Fukuoka, S.

Biosci. Biotechnol. Biochem. 58, 1282-1285, 1994

A:Title: Analysis of ZAPs, zymogen granule membrane associated proteins, in the regulate

A:Reference number: PC2195; MUID:94362286; PMID:7765250

A:Accession: PC2195

A:Molecule type: protein

A:Residues: 22-32 <FUK>

A:Experimental source: pancreas

A:Note: This sequence is identical to that of glycoprophosphatidylinositol (GPI)-anchored p

C:Comment: This protein localizes in the zymogen granule membrane and has important func

C:Superfamily: membrane glycoprotein 2; membrane glycoprotein 2 homology; ZP domain hom

C:Keywords: calcium binding; glycoprotein; lipoprotein; membrane protein; pancreas; phos

F:34-50/Domain: membrane glycoprotein 2 homology <MGH>

F:200-450/Domain: ZP domain homology <ZPH>

Query Match 12.0%; Score 210; DB 1; Length 509;

Best Local Similarity 25.9%; Pred. No. 3.7e-10;

Matches 72; Conservative 43; Mismatches 115; Indels 48; Gaps 10;

Qy 32 CYPKTIITKIPCPYGVHQLALGGLCYNGVHEGGYQFVLPDL----- 76

Db 201 CGAKEIQVSLDKC-----QLGGL-----GFGDEVIAIYLRDWNCSNMQRERN 243

Qy 77 -----SPKNKSYCGTQSEYKPIYHFYSHIVSNDDTVIVKNQPVNYSFCTVHSTYLVN- 130

Db 244 WLSVTSPTQARACGNILE--RNQTHAIYKNTLSLANEFTIRDLININFCAYPLDMKVS 302

Qy 131 QAAFDQVATVHVXNGSMGTFFESQLSLNFYTNKAFSIKKEAPFVLEASIGSDLFAG-VE 189

Db 303 QPALHPVSSLNISVDGEGFTVRMAL--FDQSYISPYEGAAVL--AVESMLVVGAIL 358

Qy 190 AKGLSIRFKVNLNSCWATPSADPMYPLQWLKNGCPT--DPTVLVHNGRDHRAFPQ 247

Db 359 EKGDTSRFLLRNLCYATPTKDTFVKYFIIRNSCPNQYDSTIHVEENGSSERFSVQ 418

Qy 248 AFRFQNIPLSKVWLHCETFCIDSEKLSCPVTCDEKRLR 285

Db 419 MEFVAG--NYDLVFLHCEIHLCDLSLNEQCQPCCSRQ 454

RESULT 9

G02091

pancreatic zymogen granule membrane protein GP-2 - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 21-Jan-2000

C:Accession: G02091

R:Wong, S.M.E.; Lowe, A.W.

submitted to the EMBL Data Library, September 1995

A:Reference number: H00789

A:Accession: G02091

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-530 <WON>

A:Cross-references: EMBL:U36221; NID:g1244511; PIDN:AAB19240.1; PID:g1244512

C:Superfamily: membrane glycoprotein 2; membrane glycoprotein 2 homology; ZP domain hom

F:55-530/Domain: membrane glycoprotein 2 homology <MGH>

F:221-471/Domain: ZP domain homology <ZPH>

Query Match 12.0%; Score 210; DB 2; Length 530;

Best Local Similarity 26.8%; Pred. No. 4e-10;

Matches 75; Conservative 43; Mismatches 104; Indels 58; Gaps 11;

Qy 32 CYPKTIITKIPCPYGVHQLALGGLCYNGVHEGGYQFVLPDL----- 76

Db 222 CGPREIKVYDKC-----LLGGL-----GLGEEVIAYLRDPNCSILQTERN 264

Qy 77 -----SPKNKSYCGTQSEYKPIYHFYSHIVSNDDTVIVKNQPVNYSFCTVHSTYLVN- 130

Db 265 WSVTSPTQASACRNILE--RNQTHAIYKNTLSLVNDFIIRDITLININFCAYPLDMKVS 323

Qy 131 QAAFDQVATVHVXNGSMGTFFESQLSL--NFYTNKAFSIKKEAPFVLEASIG--SDLF 185

Db 324 QAAQLQPVSSLNISVDGEGFTVRMALFDQNYTN-----PYEGDAVELSVESVLY 374

Qy 186 AG-VEAKGLSIRFKVNLNSCWATPSADPMYPLQWLKNGCPT--DPTVLVHNGRDHRA 242

Db 375 VGAILEQDTSRFLNLRNLCYATPTEDKADLVKFIIRNSCSNORDSTIHVEENGSS 434

Qy 243 TFQENAFRQNIPLSKVWLHCETFCIDSEKLSCPVTCDK 282

Db 435 RFSVQMFAGHYDL--VFLHCEIHLCDLSLNEQCQPCCSR 472

RESULT 10

alpha tectorin - chicken

C:Species: Gallus gallus (chicken)

C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

C:Accession: T30243

R:Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.

Hear. Res. 130, 62-74, 1999

A:Title: Chick alpha tectorin : molecular cloning and expression during embryogenesis.

A:Reference number: 220783; MUID:99251817; PMID:10320099

A:Accession: T30243

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2120 <COU>

A:Cross-references: UNIPROT:Q9VH85; EMBL:AJ012287; NID:e1361091; PID:e1361092; PIDN:CAAO

A:Note: non-collagenous protein only expressed in the inner ear

Query Match 11.6%; Score 204; DB 2; Length 2120;

Best Local Similarity 24.3%; Pred. No. 7.7e-09;

Matches 77; Conservative 48; Mismatches 128; Indels 64; Gaps 14;

Qy 30 VFCYKTIITKIPSC---PYGMEVHQLALGGLCYNGVHEGGYQFVLPDLSPKNKSYCG- 85

Db 1771 VTCAAQMEVSIKCKLFGQFEGREGVRVNDRHCPGIEGEDFISFQINN-----TKNGCN 1826

Qy 86 -----TQSEYKPIYHFYSHIVSNDDTVIVKNQPVNYSFCTVHSTYLVNQAAPDQV- 138

Db 1827 LVQSNSTHIVYKNTV---WIESANNNGNIITRDRTINVEVFCAYE--LDIKISLDSVVR 1880

Qy 139 -----ATVHVXNGSMGTFFESQLSLNFYTNKAFSIK-KEAPFVLEASIGSDLFAGVEA 190

Db 1881 PMLSVINLTVPTQEGS---FTTKMAL--YKNSSYKHPYRQGEVLTTRDV---LVGVFV 1932

QY 191 KGL-SIRPKVILNSCWATPSADFMYPLOWOLINKGCP--DETVLVHNGRDRHATFQFN 247
Db 1933 VGADSNHLILMLNKCAYATPGRSDNDKLRYPFIIEGGQNLKNDTIGIEENGVSITCRFHYT 1992
QY 248 AFRFONIPKLSKVLWHLCHETICDSEKSLCPVTCDKRRLLRDQTGGVVLVVELSLRSRGFS 307
Db 1993 VFKE--IGDYDEVHLHCANSLCDSEKYSCKINCPQHR----- 2028
QY 308 SLYSFSDVLHLLIMLG 324
Db 2029 SASAFAQEAHEQILSVG 2045
RESULT 11
T42721
CRP-ductin-alpha precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42721
R;Cheng, H.; Bjerknes, M.; Chen, H.
Anat. Rec. 244, 327-343, 1996
A;Title: CRP-ductin: a gene expressed in intestinal crypts and in pancreatic and hepatic
A;Reference number: Z22241; MUID:96362470; PMID:8742698
A;Accession: T42721
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2083 <CHE>
A;Cross-references: UNIPROT:Q60997; EMBL:U37438; NID:g1276646; PID:g1276647; PIDN:AAC525
A;Experimental source: strain BALB/c; jejunal epithelial cells
C;Keywords: transmembrane protein
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-2083/Product: CRP-ductin-alpha #status predicted <MAT>
Query Match 8.6%; Score 150.5; DB 2; Length 2083;
Best Local Similarity 24.0%; Pred. No. 0.0003;
Matches 47; Conservative 46; Mismatches 76; Indels 27; Gaps 10;
QY 84 CGT--QSEYKPIY-HFYSHIVSNDTTLVKNQPNVYFSC-----TYHST-YLVNQAP 134
Db 1803 CGTIKQADNETINYNFLRAWNSG--IIXRRDLNIHVSCKMLQNTWNTWYITNN--- 1857
QY 135 DORVATVHVKNVSGMGTFFESOLNIFYTNAKFSIK-KEAPFVLEASEIGSDLPAGVEAKGL 193
Db 1858 -----IVIEIQVQYGNF--VNISFYTSSFLFPVTSSPYV---DLQNLVLQAEILHS 1907
QY 194 SIRPKVILNSCWATPSADFMYPLOWOLINKGCPDETTLVHNGRDRHATFQFNAPFQFN 253
Db 1908 DASLALFVDTCVASPHNPDPFSSLTLDLRSGCVRDDTYQSYSPSPRVRFRKFFSFFHFLN 1967
QY 254 IPKLSKVLWHLCHETIFC 269
Db 1968 --RFPSSVYLQCKLWVC 1981
RESULT 12
A59386
sanko - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004
C;Accession: A59386
R;sanko, S.
submitted to the Protein Sequence Database, March 2001
A;Reference number: A59386
A;Accession: A59386
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-2403 <SAN>
A;Cross-references: UNIPROT:Q9UGM2
Query Match 8.6%; Score 150.5; DB 2; Length 2403;
Best Local Similarity 23.2%; Pred. No. 0.00036;
Matches 64; Conservative 47; Mismatches 102; Indels 63; Gaps 15;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:22:12 ; Search time 169 Seconds
(without alignments)
996.888 Million cell updates/sec

Title: US-10-687-268-35

Perfect score: 1756

Sequence: 1 MVTKAFVLLAFAEASAKSC.....YSFSDVLLHLMMLGICAVL 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_treml:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1756	100.0	329	1	TECB_HUMAN
2	1665	94.8	329	1	TECB_MOUSE
3	1357.5	77.3	329	1	TECB_CHICK
4	251	14.3	415	2	Q95J36
5	250	14.2	431	2	Q8TCW7
6	247	14.1	415	2	Q8BGZ8
7	247	14.1	415	2	Q661R0
8	237	13.5	534	2	Q9D733
9	235.5	13.4	642	2	Q862Z3
10	230	13.1	2155	1	TECA_MOUSE
11	229.5	13.1	573	2	Q9D6X7
12	228.5	13.0	644	1	UROM_RAT
13	228.5	13.0	644	2	Q642D6
14	224	12.8	642	2	Q62285
15	223.5	12.7	642	2	Q91X17
16	221	12.6	2155	1	TECA_HUMAN
17	220	12.5	643	1	UROM_BOVIN
18	219	12.5	507	2	Q6ZS84
19	219	12.5	611	2	Q81YGO
20	219	12.5	640	1	UROM_HUMAN
21	216	12.3	530	1	GP2_RAT
22	213	12.1	380	2	Q8NIA3
23	210	12.0	509	1	GP2_CANFA
24	210	12.0	527	1	GP2_HUMAN
25	210	12.0	530	2	Q6BD34
26	204	11.6	2120	1	TECA_CHICK
27	202	11.5	797	2	Q8UW62
28	184.5	10.5	606	2	P70412
29	183	10.4	211	2	Q9CV56
30	182	10.4	413	2	Q8BYD5
31	181.5	10.3	607	2	O35360

32	181.5	10.3	607	2	Q9QZT0
33	178.5	10.2	1246	2	O6LA40
34	178.5	10.2	1374	2	O6LA41
35	178	10.1	429	2	Q91650
36	175.5	10.0	418	2	Q766V2
37	174	9.9	457	2	Q72660
38	172	9.8	375	2	Q8AWX2
39	172	9.8	457	2	Q72661
40	172	9.8	607	2	Q86UP6
41	171	9.7	272	2	Q8N216
42	171	9.7	326	2	Q86SG1
43	167	9.5	905	2	Q919R5
44	164	9.3	149	2	Q9CV52
45	164	9.3	357	2	Q9HAR7

Q9qzt0 rattus norv
Q6la40 homo sapien
Q6la41 homo sapien
Q91650 xenopus lae
Q766v2 gallus gall
Q72660 homo sapien
Q8awx2 xenopus tro
Q72661 homo sapien
Q86up6 homo sapien
Q8n216 homo sapien
Q86sg1 homo sapien
Q919r5 xenopus lae
Q9cv52 mus musculu
Q9har7 homo sapien

ALIGNMENTS

RESULT 1
TECB_HUMAN
ID: Q96PI2; STANDARD; PRT; 329 AA.
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-tectorin precursor.
GN Name=TECB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Xia J.H., Zhang H.L., Deng H., Lu C.Y., Pang Q.;
RT "Cloning and identification of human TECB.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: One of the major non-collagenous components of the tectorial membrane (By similarity). The tectorial membrane is an extracellular matrix of the inner ear that covers the neuroepithelium of the cochlea and contacts the stereocilia bundles of specialized sensory hair cells. Sound induces movement of these hair cells relative to the tectorial membrane, deflects the stereocilia and leads to fluctuations in hair-cell membrane potential, transducing sound into electrical signals.
CC -!- SUBUNIT: May form homomeric filament after self-association or heteromeric filament after association with alpha-tectorin.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (Probable). Found in the non-collagenous matrix of the tectorial membrane (By similarity).
CC -!- DOMAIN: Zona pellucida domain may enable to form filaments.
CC -!- PTM: The presence of a hydrophobic C-terminus preceded by a potential cleavage site strongly suggests that tectorins are synthesized as glycosylphosphatidylinositol-linked, membrane-bound precursors. Tectorins are targeted to the apical surface of the inner ear epithelia by the lipid and proteolytically released into the extracellular compartment.
CC -!- SIMILARITY: Contains 1 ZP domain.

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EMBL; AF312827; AAL12829.1; -
Genew; HGNC:11721; TECB.
MIM; 602653; -
InterPro; IPR001507; Endoglin/CD105.
Pfam; PF00100; Zona_pellucida; 1.


```
DR PRINTS: PR00023; ZPELLUCIDA.
DR SMART: SM00241; ZP: 1.
DR PROSITE: PS00682; ZP_DOMAIN; FALSE_NEG.
KW Extracellular matrix; Glycoprotein; GPI-anchor; Lipoprotein; Membrane;
FT SIGNAL.
FT CHAIN 1 17 Potential.
FT PROPEP 18 305 Beta-tectorin.
FT DOMAIN 19 283 Removed in mature form (Potential).
FT LIPID 305 305 ZP.
FT CARBOHYD 80 80 GPI-anchor amidated glycine (Potential).
FT CARBOHYD 104 104 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 116 116 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 145 145 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 329 AA; 36955 MW; 0B4D379624F48D0 CRC64;

Query Match 100.0%; Score 1756; DB 1; Length 329;
Best Local Similarity 100.0%; Pred. No. 5.9e-146;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTKAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGEVHQLAGGLCY 60
DB 1 MVTKAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGEVHQLAGGLCY 60
QY 61 NGVHEGGYQFVLPDLSPKNKSYCGTQSEYKPPYHVFYSHIVSNDTIVKQNPVNSFS 120
DB 61 NGVHEGGYQFVLPDLSPKNKSYCGTQSEYKPPYHVFYSHIVSNDTIVKQNPVNSFS 120
QY 121 CTHYSTYLVNQAAFDQVATVHVKNKSGMGTFFESQLSLNFYTNNAKFSIKKEAPFVLESEI 180
DB 121 CTHYSTYLVNQAAFDQVATVHVKNKSGMGTFFESQLSLNFYTNNAKFSIKKEAPFVLESEI 180
QY 181 GSDLFAGVEAKGLSTRFKVVLNSCWATPSADPMYPLQWLKNGCPTDVTVLVHNGRDH 240
DB 181 GSDLFAGVEAKGLSTRFKVVLNSCWATPSADPMYPLQWLKNGCPTDVTVLVHNGRDH 240
QY 241 RATQFNQAFNRFQNIPLKSKVWLHCETFCIDSEKLSKCPVTCDDRKLRLRDOTGGVLVVELS 300
DB 241 RATQFNQAFNRFQNIPLKSKVWLHCETFCIDSEKLSKCPVTCDDRKLRLRDOTGGVLVVELS 300
QY 301 LRSRGFSSLSYFSDVLHLLHMLGICAVL 329
DB 301 LRSRGFSSLSYFSDVLHLLHMLGICAVL 329

RESULT 2
TECB MOUSE STANDARD; PRT; 329 AA.
AC O08524;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-tectorin precursor.
GN Name=Tectb;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Cochlea;
RX MEDLINE=97236843; PubMed=9079715; DOI=10.1074/jbc.272.13.8791;
RA Legan P.K., Rau A., Keene J.N., Richardson G.P.;
RT "The mouse tectorins. Modular matrix proteins of the inner ear
RT homologous to components of the sperm-egg adhesion system.";
RL J. Biol. Chem. 272:8791-8801(1997).
CC -!- FUNCTION: One of the major non-collagenous components of the
CC tectorial membrane (By similarity). The tectorial membrane is an
CC extracellular matrix of the inner ear that covers the
CC neuroepithelium of the cochlea and contacts the stereocilia
CC bundles of specialized sensory hair cells. Sound induces movement
CC of these hair cells relative to the tectorial membrane, deflects
CC the stereocilia and leads to fluctuations in hair-cell membrane
```

```
CC potential, transducing sound into electrical signals.
CC -!- SUBUNIT: May form homomeric filament after self-association or
CC heteromeric filament after association with alpha-tectorin.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Probable). Found in the non-collagenous matrix of the tectorial
CC membrane (By similarity).
CC -!- DOMAIN: Zona pellucida domain may enable to form filaments.
CC -!- PTM: The presence of a hydrophobic C-terminus preceded by a
CC potential cleavage site strongly suggests that tectorins are
CC synthesized as glycosylphosphatidylinositol-linked, membrane-bound
CC precursors. Tectorins are targeted to the apical surface of the
CC inner ear epithelia by the lipid and proteolytically released into
CC the extracellular compartment.
CC -!- SIMILARITY: Contains 1 ZP domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; X99806; CAA68139.2; -.
CC MGD; MGI:109574; Tectb.
CC GO; GO:0005578; C:extracellular matrix; IDA.
CC GO; GO:0005201; F:extracellular matrix structural constituent; IDA.
CC InterPro; IPR001507; Endoglin/CD105.
CC Pfam; PF00100; Zona_pellucida; 1.
CC PRINTS; PR00023; ZPELLUCIDA.
CC SMART; SM00241; ZP; 1.
CC PROSITE; PS00682; ZP_DOMAIN; FALSE_NEG.
KW Extracellular matrix; Glycoprotein; GPI-anchor; Lipoprotein; Membrane;
FT SIGNAL.
FT CHAIN 1 17 Potential.
FT PROPEP 18 305 Beta-tectorin.
FT DOMAIN 19 283 Removed in mature form (Potential).
FT LIPID 305 305 ZP.
FT CARBOHYD 80 80 GPI-anchor amidated alanine (Potential).
FT CARBOHYD 104 104 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 116 116 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 145 145 N-linked (GlcNAc. .) (Potential).
SQ SEQUENCE 329 AA; 36985 MW; CC69A33BEC270AB3 CRC64;

Query Match 94.8%; Score 1665; DB 1; Length 329;
Best Local Similarity 94.2%; Pred. No. 5.9e-138;
Matches 310; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MVTKAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGEVHQLAGGLCY 60
DB 1 MVTKAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGEVHQLAGGLCY 60
QY 61 NGVHEGGYQFVLPDLSPKNKSYCGTQSEYKPPYHVFYSHIVSNDTIVKQNPVNSFS 120
DB 61 NGVHEGGYQFVLPDLSPKNKSYCGTQSEYKPPYHVFYSHIVSNDTIVKQNPVNSFS 120
QY 121 CTHYSTYLVNQAAFDQVATVHVKNKSGMGTFFESQLSLNFYTNNAKFSIKKEAPFVLESEI 180
DB 121 CTHYSTYLVNQAAFDQVATVHVKNKSGMGTFFESQLSLNFYTNNAKFSIKKEAPFVLESEI 180
QY 181 GSDLFAGVEAKGLSTRFKVVLNSCWATPSADPMYPLQWLKNGCPTDVTVLVHNGRDH 240
DB 181 GSDLFAGVEAKGLSTRFKVVLNSCWATPSADPMYPLQWLKNGCPTDVTVLVHNGRDH 240
QY 241 RATQFNQAFNRFQNIPLKSKVWLHCETFCIDSEKLSKCPVTCDDRKLRLRDOTGGVLVVELS 300
DB 241 RATQFNQAFNRFQNIPLKSKVWLHCETFCIDSEKLSKCPVTCDDRKLRLRDOTGGVLVVELS 300
QY 301 LRSRGFSSLSYFSDVLHLLHMLGICAVL 329
DB 301 LRSRGFSSLSYFSDVLHLLHMLGICAVL 329
```

RESULT 3
TECB CHICK STANDARD; PRT; 329 AA.
AC P54097;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-tectorin precursor.
GN Name=TECB;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RC STRAIN=Isa brown; TISSUE=Cochlear duct;
RX MEDLINE=95238547; PubMed=7721949; DOI=10.1083/jcb.129.2.535;
RA Killick R., Legan P.K., Malenczak C., Richardson G.P.;
RT "Molecular cloning of chick beta-tectorin, an extracellular matrix
molecule of the inner ear."
RL J. Cell Biol. 129:535-547(1995).
RN [2]
RP FUNCTION.
RX PubMed=1490898; DOI=10.1016/0378-5955(92)90165-J;
RA Killick R., Malenczak C., Richardson G.P.;
RT "The protein composition of the avian tectorial membrane."
RL Hear. Res. 64:21-38(1992).
RN [3]
RP TISSUE SPECIFICITY.
RX STRAIN=White leghorn;
RA MEDLINE=98409669; PubMed=9736748; DOI=10.1073/pnas.95.19.11400;
RA Heller S., Sheane C.A., Javed Z., Hudspeth A.J.;
RT "Molecular markers for cell types of the inner ear and candidate genes
for hearing disorders."
RL Proc. Natl. Acad. Sci. U.S.A. 95:11400-11405(1998).
RN [4]
CC -!- FUNCTION: One of the major non-collagenous components of the
CC tectorial membrane. The tectorial membrane is an extracellular
CC matrix of the inner ear that covers the neuroepithelium of the
CC cochlea and contacts the stereocilia bundles of specialized
CC sensory hair cells. Sound induces movement of these hair cells
CC relative to the tectorial membrane, deflects the stereocilia and
CC leads to fluctuations in hair-cell membrane potential, transducing
CC sound into electrical signals.
CC -!- SUBUNIT: May form homomeric filament after self-association or
CC heteromeric filament after association with alpha-tectorin.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Probable). Found in the non-collagenous matrix of the tectorial
CC membrane (by similarity).
CC -!- TISSUE SPECIFICITY: Exclusively expressed in the inner ear, where
CC it is found in basilar papilla, clear cells, supporting cells,
CC cuboidal cells and the lagena macula.
CC -!- DOMAIN: Zona pellucida domain may enable to form filaments.
CC -!- PTM: The N-terminus is blocked.
CC -!- PTM: N-glycosylated.
CC -!- PTM: The presence of a hydrophobic C-terminus preceded by a
CC potential cleavage site strongly suggests that tectorins are
CC synthesized as glycosylphosphatidylinositol-linked, membrane-bound
CC precursors. Tectorins are targeted to the apical surface of the
CC inner ear epithelia by the lipid and proteolytically released into
CC the extracellular compartment.
CC -!- SIMILARITY: Contains 1 ZP domain.

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CC or send an email to license@isb-sib.ch).

CC EMBL; L38519; AAA92461.1; -.

DR PIR; A57246; A57246.
DR InterPro; IPR001507; Endoglin/CD105.
DR InterPro; IPR008975; Viral cap coat.
DR Pfam; PF00100; zona_pellucida; 1.
DR PRINTS; PRO0023; ZPELLUCIDA.
DR SMART; SM00241; ZP; 1.
DR PROSITE; PS00682; ZP_DOMAIN; 1.
KW Extracellular matrix; Glycoprotein; GPI-anchor; Lipoprotein; Membrane;
FT SIGNAL.
FT CHAIN.
FT CHAIN 1 17 Potential.
FT CHAIN 18 304 Beta-tectorin.
FT PROPEP 305 329 Removed in mature form (Potential).
FT DOMAIN 91 283 ZP.
FT LIPID 304 304 GPI-anchor amidated glycine (Potential).
FT CARBOHYD 80 80 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 104 104 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 116 116 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 329 AA; 36899 MW; 4D66131C733C0DA2 CRC64;
Query Match 77.3%; Score 1357.5; DB 1; Length 329;
Best Local Similarity 73.6%; Pred. No. 6.4e-111;
Matches 242; Conservative 44; Mismatches 42; Indels 1; Gaps 1;
QY 1 MVTKAFVLLAIFAEASAKSCAPNKADVLVFCYPTKIITKIPECPYGEVHQLALGLCY 60
Db 1 MVAVTVLWVLAQAFAAGPCTPNKADVLVVCYPTKIITKIPECPYGEVHQLALGLCY 60
QY 61 NGVHEGGYQVPIPDLPKNSYCGTSEYKPPYHYFVSHVSNDDTVIVKQNPVNSFS 120
Db 61 NGIHDSGYQFTIPDLSPKNSYCGTSEYKPPYHYFVSHVSNDDTVIVKQNPVNSFS 120
QY 121 CTYHSTVLVNOAARDQVATVHVNGSGMTGSPESQLSLNFYTNKFSIKKEAPFVLESEI 180
Db 121 CTYANVVLVNOAARDQVATVHVNGSGMTGSPESQLSLNFYTNKFSIKKEAPFVLESEI 180
QY 181 GSDIFAGVEAKGLSIRFKVVLNSCWATPSPADFMYPLOQLINKGCPDDETVLVHENGDRH 240
Db 181 GSDIFAGVEAKGLSIRFKVVLNSCWATPSPADFMYPLOQLINKGCPDDETVLVHENGDRH 240
QY 241 RATQFNAFRQNPQIKSLKWLHCETFDSEKLSCTPCTDKRRLLRDQGGVVLVLS 300
Db 241 RATQFNAFRQNPQIKSLKWLHCETFDSEKLSCTPCTDKRRLLRDQGGVVLVLS 300
QY 301 LRSQGSLSYFSFVSLHLLIMLGLICAVL 329
Db 300 VRNKGSLRFRYMLSDVIFHLLFAIGFCAIL 328
RESULT 4
QY 95J36 PRELIMINARY; PRT; 415 AA.
AC QY5J36;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
RA Terao K., Sugano S., Hashimoto K.;
RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
in the human genome sequence."
RL BMC Genomics 3:36-36(2002).
DR InterPro; IPR001507; Endoglin/CD105.
DR Pfam; PF00100; zona_pellucida; 1.

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Ogawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck, Head, and
RC Kidney;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Koyama S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK034628; BAC28777.1; -;
DR EMBL; AK047981; BAC33205.1; -;
DR EMBL; AK052599; BAC35056.1; -;
DR MGD; MGI:2443415; 9430016A21Rik.
DR GO; GO:0016021; C.integral to membrane; TAS.
DR InterPro; IPR001507; Endoglin/CD105.
DR Pfam; PF00100; Zona_pellucida; 1.
DR PRINTS; PR00023; ZPELLUCIDA.
DR SMART; SM00241; ZP; 1.
KW Hypothetical protein.
SQ SEQUENCE 415 AA; 45447 MW; 5ED1871A4E257CA1 CRC64;
Query Match 14.1%; Score 247; DB 2; Length 415;
Best Local Similarity 27.8%; Pred. No. 3.7e-13;
Matches 83; Conservative 46; Mismatches 136; Indels 34; Gaps 11;
QY 14 EASAKSCAPNKADVILVFCYKPTIITKIPECY---GWEVHOLALGGL-----CYNGVHE 65
DB 27 DANLHRSRFAERD-ISVYGVQVQAITWKINFCVLSGYSETDLNGRUGDHSRGRFINN 85
QY 66 GGYQYQVPIPLSPKPKNSCYGQTQ-----SEYKPIYHYFYSHIVSNDTTIVKVN 112
DB 86 NTFFPAVVIIFINLSTLEGCGNNLVSTIPGVGASGNATTVOIGNISGYIDTDPDPAVISY 145
QY 113 QP-VNYSFCTHSTYLVNQAAFDQQRVATVHVKNVSGMGTFESQLSINFTYTNKAFSIKKEA 171
DB 146 LPGLLYKFCSCYPLEYLVNNTQLASSAAISVRENN-GTFVSTLNLLYNDSTYREQLII 204
QY 172 PFVLEASIGSLFAGVEAKGISIRFKVLNVCWATPSADFMYPQLQWLINKGCPDTEV 231
DB 205 PSI--GLPLTKVFAVQATNLDGRWNVLMDYCYTTPSGNPNDDTYIDLF-LSCDKDPOT 261
QY 232 LVHENGDRHRAVQFNAFRF--QNIPLKSLVHLHCETFTCDSEKLSCPV---TCDKRRK 285
DB 262 TWIENGSRQGRFSFEVFFVFKHQNQMSTVFLHCLTKLCRAD--DCPLLMPICGNRKR 318
RESULT 7
Q66IRO PRELIMINARY; PRT; 415 AA.
AC Q66IRO;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE MGC85537 protein.
GN Name=MGC85537;

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_taxid=83355;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S., Gerhardt D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081237; AAH81237.1; -;
DR InterPro; IPR001507; Endoglin/CD105.
DR InterPro; IPR006162; Ppanth S.
DR InterPro; IPR010916; TONB_Box_N.
DR Pfam; PF00100; Zona_pellucida; 1.
DR PRINTS; PR00023; ZPELLUCIDA.
DR SMART; SM00241; ZP; 1.
DR PROSITE; PS00012; PHOSPHOPANTHINE; UNKNOWN 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN 1.
SQ SEQUENCE 415 AA; 45730 MW; 3787133B98507169 CRC64;
Query Match 14.1%; Score 247; DB 2; Length 415;
Best Local Similarity 27.5%; Pred. No. 3.7e-13;
Matches 88; Conservative 47; Mismatches 135; Indels 50; Gaps 13;
QY 7 VLLAIF-----AEASAKSCAPNKADVILVFCYKPTIITKIPECY---GWEVH 51
DB 8 LLLAIFTVSVAQFNQYNCANDANQHSRFAERD-ITVYGVQVITWKINFCVLSGYSES 66
QY 52 QIALGGL-----CYNGVHEGYQYQVPIPLSPKPKNSYC-----GTQSEYK 91
DB 67 DLSLNGKHGDAHCRGFNNNTFPVITFTNLSTLSCNSLVSTVPGVNAYGIASMVQ 126
QY 92 PPIVHFYSHIVSNDTTIVKVNQ--VNYSFCTHSTYLVNQAAFDQQRVATVHVKNVSGMT 150
DB 127 --IGNISGYIDTDPPTIISYLVPLGLLYKFCSCYPLEYLVNNTQLASSAAISVREGN-GT 183
QY 151 FESQLSLNFTYTNKAFSIKKEAPFVLEASIGSLFAGVEAKGLSIRFKVLNVCWATPSA 210
DB 184 FISTLNLLYNDSTYSQQLLIPSA--GLPLTKIYAAVRATNLDGRWNVLMDYCYTTPSG 241


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DR InterPro; IPR001507; Endoglin/CD105.
DR Pfam; PF07645; EGF CA; 2.
DR Pfam; PF00100; Zona_pellucida; 1.
DR PRINTS; PR00023; ZPELLUCIDA.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00241; ZP; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00682; ZP_DOMAIN; 1.
DR EGF-like domain.
KW EGF-like domain.
SQ SEQUENCE 642 AA; 70177 MW; 608ACCF13A667E64 CRC64;

Query Match
Best Local Similarity 13.4%; Score 235.5; DB 2; Length 642;
Matches 84; Conservative 62; Mismatches 140; Indels 57; Gaps 12;

QY 2 VTKAFVLLAFAEASAKSNKADVLVFCYPKTIITKIPECPYGEVHQLAGGLCVN 61
DB 325 VTDLFLL-----DELCRPNDIKVLSKQKSL-----GFEKVFYLRDSQCS 368

QY 62 GVHEGYOYFVDPIDSPKNSVCGTQSEYKPIYHYFVSHVNSDFTTVIVKNQPVNYSFSC 121
DB 369 GFNERGDRDW-SVTPARDGPGCTVM-VRNETHATYSNTLYLADBEIVIRDRNIKINFE 426

QY 122 TYHSTYLVN-QAADFQVATVHVKNMGCTPFESQSL-----NFYTNKFSIKKEAPF 173
DB 427 SYPLDMKVSLETSLQPIVSSLSINVGVTGMFTVRMALFQTPDYTPQYQSSVTLTTEAF 486

QY 174 VLEASIEGDLFAGVEAKGLSIRFKVLNLSWATPSADPMYFLOWLKNKGC--TDFTV 231
DB 487 YGTWLDGGLD-----SRFALLMNCVATSSNATDPLKFIIDRCPTIDSTI 536

QY 232 LVHENGDRHRAVTFQNAFQNIPLSKVWLHCETFCIDSEKSLCPVTCRKRLLRDTQ 291
DB 537 QVVENGESQGRFSVQMFREAG--NYDLVYLHCEVVLGDCIINEKCKPTCSG---TRFS 590

QY 292 GGVV-----VVEL-----SLRSGFSLSYFSDVLHLIM 321
DB 591 GGIIDQSRVNLGPIITRKNVQAVWSRASSSIGFLKVLPLLL 633

RESULT 10
TECA MOUSE
ID TECA MOUSE STANDARD; PRT; 2155 AA.
AC O08523;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alpha-tectorin precursor.
GN Name=Tecta;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF 25-34, SUBUNITS,
RP SUBCELLULAR LOCATION, POST-TRANSLATIONAL MODIFICATIONS, AND TISSUE
RP SPECIFICITY.
RC STRAIN=CD-1; TISSUE=Cochlea;
RX MEDLINE=97236843; PubMed=9079715; DOI=10.1074/jbc.272.13.8791;
RA Legan P.K., Rau A., Keene J.N., Richardson G.P.;
RT "The mouse tectorins. Modular matrix proteins of the inner ear
RT homologous to components of the sperm-egg adhesion system.";
RL J. Biol. Chem. 272:8791-8801(1997).
RN [2]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=98250172; PubMed=9590290;
RA Verhoeven K., Van Laer L., Kirschhofer K., Legan P.K., Hughes D.C.,
RA Schattman I., Verstrecken M., Van Hauwe P., Coucke P., Chen A.,
RA Smith R.J.H., Somers T., Offeciers F.E., Van de Heyning P.,

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RA Richardson G.P., Wachtler F., Kimberling W.J., Willems P.J.,
RA Govaerts P.J., Van Camp G.;
RT "Mutations in the human alpha-tectorin gene cause autosomal dominant
RT non-syndromic hearing impairment.";
RL Nat. Genet. 19:60-62(1998).
CC -!- FUNCTION: One of the major non-collagenous components of the
CC tectorial membrane (By similarity). The tectorial membrane is an
CC extracellular matrix of the inner ear that covers the
CC neuroepithelium of the cochlea and contacts the stereocilia
CC bundles of specialized sensory hair cells. Sound induces movement
CC of these hair cells relative to the tectorial membrane, deflects
CC the stereocilia and leads to fluctuations in hair-cell membrane
CC potential, transducing sound into electrical signals.
CC -!- SUBUNIT: May form homomeric filament after self-association or
CC heteromeric filament after association with beta-tectorin.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Probable). Found in the non-collagenous matrix of the tectorial
CC membrane.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O08523-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O08523-2; Sequence=VSP_010557;
CC -!- TISSUE SPECIFICITY: Cochlea-specific.
CC -!- DOMAIN: Zona pellucida domain may enable to form filaments.
CC -!- PTM: 3 products of tectorin seem to exist: HMM, MMM and LMM. They
CC may be generated by active processing or the result of proteolysis
CC occurring between intrachain disulfid bonds.
CC -!- PTM: The presence of a hydrophobic C-terminus preceded by a
CC potential cleavage site strongly suggests that tectorins are
CC synthesized as glycosylphosphatidylinositol-linked, membrane-bound
CC precursors. Tectorins are targeted to the apical surface of the
CC inner ear epithelia by the lipid and proteolytically released into
CC the extracellular compartment.
CC -!- SIMILARITY: Contains 1 NIDO (nidogen-like) domain.
CC -!- SIMILARITY: Contains 3 TIL (Trypsin inhibitory-like) domains.
CC -!- SIMILARITY: Contains 1 VWFC domain.
CC -!- SIMILARITY: Contains 4 VWFD domains.
CC -!- SIMILARITY: Contains 1 ZP domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; X99805; CAA68138.1; -.
DR PIR; T30197; T30197.
DR HSP; P56682; ICCV.
DR MGD; MGI:109575; Tecta.
DR GO; GO:0005578; C:extracellular matrix; IDA.
DR GO; GO:0005201; F:Extracellular matrix structural constituent; IDA.
DR InterPro; IPR002086; Aldehyde dehydr.
DR InterPro; IPR002919; Cysrich_TIL.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001507; Endoglin/CD105.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR006210; IEGF-.
DR InterPro; IPR010362; NIDO.
DR InterPro; IPR003886; Nidogen_ext.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF06119; NIDO; 1.
DR Pfam; PF01826; TIL; 3.
DR Pfam; PF00094; VWD; 4.
DR Pfam; PF00100; Zona_pellucida; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00539; NIDO; 1.
DR SMART; SM00214; VWC; 1.
DR SMART; SM00216; VWD; 4.

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DR SMART: SM00241; 2P: 1.
DR PROSITE, PS00184; VWFC 2; FALSE_NEG.
DR PROSITE, PS00682; ZP_DOMAIN; 1.
KW Alternative splicing; Direct protein sequencing; Extracellular matrix;
KW Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Repeat; Signal.
FT SIGNAL 1 24
FT CHAIN 25 2091 Alpha-tectorin.
FT PROPEP 2092 2155 Removed in mature form (Potential).
FT LIPID 2091 2091 GPI-anchor amidated asparagine (Potential).
FT DOMAIN 98 254 NIDO.
FT DOMAIN 260 314 VWFC.
FT DOMAIN 322 478 VWFD 1.
FT DOMAIN 597 650 TIL 1.
FT DOMAIN 713 866 VWFD 2.
FT DOMAIN 984 1036 TIL 2.
FT DOMAIN 1100 1258 VWFD 3.
FT DOMAIN 1372 1425 TIL 3.
FT DOMAIN 1487 1639 VWFD 4.
FT DOMAIN 1805 2059 ZP.
FT CARBOHYD 34 34 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 187 215 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 215 217 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 278 278 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 455 455 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 506 506 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 528 528 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 560 560 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 670 670 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 687 687 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 813 813 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 843 843 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 855 855 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 898 898 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 920 920 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 931 931 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 949 949 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1048 1048 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1064 1064 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1235 1235 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1364 1364 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1538 1538 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1565 1565 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1756 1756 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1772 1772 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1794 1794 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1851 1851 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1864 1864 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1880 1880 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1920 1920 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1939 1939 N-linked (GlcNAc. .) (Potential).
FT VARSPIC 1659 1663 Missing (in isoform 2).
SQ SEQUENCE 2155 AA; 239535 MW; 86C5C09AA392B1C5 CRC64;
Query Match 13.1%; Score 230; DB 1; Length 2155;
Best Local Similarity 27.5%; Pred. No. 8.8e-11;
Matches 80; Conservative 43; Mismatches 124; Indels 44; Gaps 14;
QY 23 NKADVT--LVFCVPKTIITKIPEC---PYGWEVHOLALGGLCYNGHEGGYQFVIPDL 77
1795 NSHDIIDAEVTKCAQMEVSIKCKLFQGFREGVRINDROCSGLIEGDFISFOINN-- 1852
DB 78 PKNKSYC-----GTQSYKPPPIYHYSHIVNSDTTIVKNQPNVNYGFSCTHYTYLVN 130
1853 --TKGCGNIVQSNTHGYKNTI---WIESANNTGNIITRDTINVEFSAYE---LDI 1904
QY 131 QAPDQV-----ATVHVNGSMGTPESQSLNFTYNAKFSIK-KEAPTFLASEIG 181
1905 KISLDSVVKPMLSVINLTVPTQEGS---FTTKVAL--YKNASYKHYPQGEVVLTRDV- 1958
QY 182 SOLFAGVEAKGL-SIRFKVVLNSCWATPSADPFMYPLQWOLINKGCPT--DETVLVHNGR 238

Db 1959 --LYGVGVVVGADSTHLTLTKCYATPSSRDSNKLRYFIIEGGCQCNKNTIGIEENG 2016
QY 239 DHRATFOFNARFRQNIPLKSKVMLHCETFCDSKLSCTPVTCDKRKELLRD 289
Db 2017 SLTCRFHVTVFKF--IGDYDEVHLHCAVSLCDSEKYSCKINCQPNQSIATD 2065
RESULT 11
Q9D6X7
ID Q9D6X7 PRELIMINARY; PRT; 573 AA.
AC Q9D6X7
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310046E09 product:membrane glycoprotein 2
DE homolog.
GN Name=Gp2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RM MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RM MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RM MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RM MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,


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Db 384 VTPARDGCGTVLR--RNETHATYSNTLYLASEIIIRDINIRINFECSYPLDMKVSILKTSL 442
Qy 135 DORVATVHVKNMGMTFESQSLNFTYTNKAFSIKKEAPFVLEASIGSDLPAGVEAKGLS 194
Db 443 QPMVSALNISLGGTGKFTVQMAL--FQNPPTYQPYQGPSVLMSTE--AFLYVGTMLDGGD 498
Qy 195 I-RFKVVLNSCWATPSADFMYPLOLQINKGCP--TDETVLVHNGRDRHRATFQFNAFRF 251
Db 499 LSRFVLLMTCYATPSSNDTPVKYFIIDRCPTHEDTTIQVTENGESSQARFSIQMFRF 558

Qy 252 QNIPKLSKVLHCETFCIDSEKLSCPVTC 280
Db 559 AGNSDL--VYLHCEVYLCDTMSQCKPTC 585

RESULT 13
Q642D6 PRELIMINARY; PRT; 644 AA.
AC Q642D6;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Uromodulin.
GN Name=Umod;
OS Rattus norvegicus (Rat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081814; AAH81814.1; -.
SQ SEQUENCE 644 AA; 71016 MW; 2414261D3472ADEC CRC64;

Query Match 13.0%; Score 228.5; DB 2; Length 644;
Best Local Similarity 27.3%; Pred. No. 2.7e-11;
Matches 57; Conservative 50; Mismatches 91; Indels 11; Gaps 7;

Qy 76 LSPKNKSYCGTQSEYKPPYHYFYSIVNSDITVIVKQPNVYSFCTVHSTYLVN-QAAF 134
Db 384 VTPARDGCGTVLR--RNETHATYSNTLYLASEIIIRDINIRINFECSYPLDMKVSILKTSL 442
Qy 135 DORVATVHVKNMGMTFESQSLNFTYTNKAFSIKKEAPFVLEASIGSDLPAGVEAKGLS 194
Db 443 QPMVSALNISLGGTGKFTVQMAL--FQNPPTYQPYQGPSVLMSTE--AFLYVGTMLDGGD 498
Qy 195 I-RFKVVLNSCWATPSADFMYPLOLQINKGCP--TDETVLVHNGRDRHRATFQFNAFRF 251
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Db 499 LSRFVLLMTCYATPSSNDTPVKYFIIDRCPTHEDTTIQVTENGESSQARFSIQMFRF 558
Qy 252 QNIPKLSKVLHCETFCIDSEKLSCPVTC 280
Db 559 AGNSDL--VYLHCEVYLCDTMSQCKPTC 585

RESULT 14
Q62285 PRELIMINARY; PRT; 642 AA.
AC Q62285;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Uromodulin.
GN Name=Umod; Synonym=Tamm-Horsfall protein;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95178555; PubMed=7873609; DOI=10.1016/0167-4781(94)00240-4;
RX Prasadani K., Bates J., Badgett A., Dell M., Sukhatme V., Yu H.,
RX Kumar S.;
RT "Nucleotide sequence and peptide motifs of mouse uromodulin (Tamm-
RT Horsfall protein)-the most abundant protein in mammalian urine.";
RL Biochim. Biophys. Acta 1260:328-332 (1995).
DR EMBL; L33406; AAA73896.1; -.
DR PIR; S52111; S52111.
DR HSSP; P35555; 1EMN.
DR MGD; MGI:102674; Umod.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001507; Endoglin/CD105.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07645; EGF_CA; 2.
DR Pfam; PF00100; Zona_pellucida; 1.
DR PRINTS; PR00023; ZPELLUCIDA.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00241; ZP; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 2.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00682; ZP_DOMAIN; 1.
KW EGF-like domain.
SQ SEQUENCE 642 AA; 70839 MW; 415A7E58D3D2B1A9 CRC64;

Query Match 12.8%; Score 224; DB 2; Length 642;
Best Local Similarity 25.5%; Pred. No. 6.6e-11;
Matches 65; Conservative 58; Mismatches 118; Indels 14; Gaps 8;

Qy 76 LSPKNKSYCGTQSEYKPPYHYFYSIVNSDITVIVKQPNVYSFCTVHSTYLVN-QAAF 134
Db 384 VTPARDGCGTVLR--RNETHATYSNTLYLASEIIIRDINIRINFECSYPLDMKVSILKTSL 440
Qy 135 DORVATVHVKNMGMTFESQSLNFTYTNKAFSIKKEAPFVLEASIGSDLPAGVEAKGLS 194
Db 441 QPMVSALNISLGGTGKFTVQMAL--FQNPPTYQPYQGPSVLMSTE--AFLYVGTMLDGGD 496
Qy 195 I-RFKVVLNSCWATPSADFMYPLOLQINKGCP--TDETVLVHNGRDRHRATFQFNAFRF 251
Db 497 LSRFVLLMTCYATPSSNDTPVKYFIIDRCPTHEDTTIQVTENGESSQARFSIQMFRF 556
Qy 252 QNIPKLSKVLHCETFCIDSEKLSCPVTC--RKRLLRDTQGVVLVVELLSRGRFSS 308
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Db 557 AG--NYDLVYLCEVYLCDSSTGEQCKPTCGTRFCGNFIDQTRVNLGPIRQRQGVQA 614
Qy 309 LYSFSDVLHLLIMML 323
Db 615 SVSASSNRLLSIWL 629

RESULT 15
Q91X17
ID Q91X17 PRELIMINARY; PRT; 642 AA.
AC Q91X17
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Uromodulin (Mus musculus 0 day neonate kidney cDNA, RIKEN full-length
DE enriched library, clone:D630023M23 product:uromodulin, full insert
DE sequence).
GN Name=Umod;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frauge C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipipillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takagawa A., Takada Y., Tanaka T.,
RA Tonaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012973; AHI2973.1; -;
DR EMBL; AK085460; BAC39452.1; -;
DR PIR; S52111; S52111.
DR HSSP; P35555; 1EMN.
DR MGD; MGI:102674; Umod.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR Pfam; PF001008; EGF; 1.
DR Pfam; PF07645; EGF_CA; 2.
DR Pfam; PF00100; Zona pellucida; 1.
DR PRINTS; PR00023; ZPELUCIDA.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00241; ZP; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 2.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00266; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00682; ZP_DOMAIN; 1.
DR EGF-like domain.
KW EGF-like domain.
SQ SEQUENCE 642 AA; 70844 MW; 31B1461B4DCAE927 CRC64;

Query Match 12.7%; Score 223.5; DB 2; Length 642;
Best Local Similarity 26.3%; Pred. No. 7.3e-11;
Matches 55; Conservative 50; Mismatches 93; Indels 11; Gaps 7;
Oy 76 LSPKKNKSYCGTQSEYKPPYHYFHYSHIVNDTIVTKNQPNVNSFCTVHSTYLVN-QAAF 134
Db 382 VTPARNGFCGTGLR-RNETHATYNTLYLANAIIIRIIRIMNFCSPYLDKMLKLTSL 440
Oy 135 DQRVATVHKNKSGMTFESQLSLNFYTNKAFPSIKKEAPFVLEASEISGDLFAGVEAKGLS 194
Db 441 QPMYSALNISLGGTGKFTVRMAL--FQSPVTYQPHGQPSVLMSTE--AFLVGTMLDGGD 496

Qy	195	I-REKVLNSCWATPSADFMYPLOWLINKGP--TDETVLVHENGDRHRATQFNAFRF	251
Db	497	LSRFVLLMNCIATPSSNSTDPVKFILODSCPRTEDTIQVTENGSSQARFSVQMF	556
Qy	252	QNIPLKLSKVWLHCETFI CDSEKLSCFVTC	280
Db	557	AG--NYDLVYLHCEVYLC DSTSEQCKPTC	583

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Job time : 172 secs